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XX (BLOO-) CENT BLOOD RES INC.
 XX Carrell WC, Moore FD, Hechtman HB;
 XX WPI: 2002-139643/18.
 XX DR N-PSDB; ABA94516.
 XX Treating or preventing immunoglobulin-mediated reperfusion or ischemic
 XX injury resulting from e.g. angioplasty, stenting procedure, atherectomy or bypass
 XX administering an inhibitor of pathogenic immunoglobulin and ischemic
 XX antigen interaction.
 XX Claim 50: Page 73-74; 77pp; English.
 XX The invention provides a method of treating or preventing immunoglobulin-
 XX mediated reperfusion or ischemic injury. The method involves
 XX administering an inhibitor of an interaction between a pathogenic
 XX immunoglobulin, and an ischemic-specific antigen or a component of the
 XX complement pathway. The method is useful for treating or preventing
 XX immunoglobulin-mediated reperfusion or ischemic injury, in particular,
 XX injury that results following a naturally occurring episode, a surgical
 XX procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
 XX surgery), or in an injury that occurs in a cardiovascular tissue. The
 XX inhibitor is useful for treating or preventing reperfusion and tissue
 XX damage following reperfusion caused by a pathogenic immunoglobulin,
 XX pathogenic IgMs. The present sequence represents the light chain variable
 XX region of 22A5 IgM, a pathogenic immunoglobulin.
 XX Sequence 115 AA:
 XX Query Match 92.48; Score 526; DB 23; Length 115;
 XX Best Local Similarity 92.58; Pred. No. 1.6e-37; Indels 0; Gaps 0;
 XX Matches 98; Conservative 5; Mismatches 5;
 QY 2 IVVTQSHKFNSTSGDRVSTICKASODVGVAVDTQKPGSPKLLIYWASTRHTGVDP 61
 DB 1 IVVTQSHKFNSTSGDRVSTICKASODVGVAVDTQKPGSPKLLIYWASTRHTGVDP 60
 QY 62 FTGSGSGDTFTLTINVOSEDADYFCQVNSYPLTFGAGTMDLK 107
 DB 61 FTGSGSGDTFTLTINVOSEDADYFCQVNSYPLTFGAGTMDLK 106
 RESULT 6
 AAP40031
 AAP40031 standard; Protein: 223 AA.
 AAP40031;
 01-DEC-1991 (first entry)
 Kappa anti-carcinoembryonic antigen chain.
 Immunoglobulin; carcinoembryonic antigen.
 EP125023-A.
 14-NOV-1984.
 06-APR-1984; 84EP-0302368.
 08-APR-1993; 83US-0483457.
 (CITY) CITY OF HOPE.
 (GETH) GENTECH INC.
 Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;
 WPI, 1984-283749/46.
 DR N-PSDB; AAP40021.
 Immunoglobulin(s) produced by recombinant host cells - useful as

XX antibodies analogous to forms from mammals.
 XX Disclosure: Fig. 3; 79pp; English.
 XX The protein is encoded by the mRNA coding sequence of the cDNA fragment
 XX contained within recombinant vector pK1764. Using the vector this
 XX immunoglobulin is produced readily in pure monoclonal form. Genetic
 XX manipulations can be used to produce chimeras of variants drawing their
 XX homology from species differing from each other. Protein manipulation
 XX is also possible.
 XX Sequence 223 AA:
 XX Query Match 92.13; Score 524; DB 5; Length 223;
 XX Best Local Similarity 90.78; Pred. No. 4.4e-37; Indels 0; Gaps 0;
 XX Matches 97; Conservative 5; Mismatches 5;
 QY 1 DIVVTQSHKFNSTSGDRVSTICKASODVGVAVDTQKPGSPKLLIYWASTRHTGVDP 60
 DB 10 DIVVTQSHKFNSTSGDRVSTICKASODVGVAVDTQKPGSPKLLIYWASTRHTGVDP 69
 QY 61 FTGSGSGDTFTLTINVOSEDADYFCQVNSYPLTFGAGTMDLK 107
 DB 70 FTGSGSGDTFTLTINVOSEDADYFCQVNSYPLTFGAGTMDLK 116
 RESULT 7
 AAP80155
 ID AAP80155 standard; protein: 247 AA.
 XX AAP80155;
 XX 13-OCT-1990 (first entry)
 XX FRs and CDRs from anti-CEA monoclonal antibody.
 XX Biosynthetic Antibody Binding site (BABS): variable domain;
 XX anti-CEA monoclonal antibody; ss.
 XX Synthetic.
 XX WO8809344-A.
 XX 01-DEC-1988.
 XX 19-MAY-1988; 88WO-US01737.
 XX 21-MAY-1987; 87US-0052800.
 XX (CREA-) CREATIVE BIOMOLECULES INC.
 XX Huston JS, Oppermann H;
 XX WPI: 1988-333928/49.
 XX N-PSDB; AAP80161.
 XX Recombinant multifunctional protein - having an Ab binding site and a
 XX sequence for biological activity, ion sequestering or binding to a solid
 XX support.
 XX Disclosure; 15pp; English.
 XX Multi-functional biosynthetic protein comprising FRs and
 XX CDRs with specific binding for a tumour antigen CEA.
 XX See also AAP80171-N80192.
 XX Sequence 247 AA:
 XX Query Match 92.13; Score 524; DB 9; Length 247;
 XX Best Local Similarity 90.78; Pred. No. 4.8e-37; Indels 0; Gaps 0;
 XX Matches 97; Conservative 5; Mismatches 5;
 QY 1 DIVVTQSHKFNSTSGDRVSTICKASODVGVAVDTQKPGSPKLLIYWASTRHTGVDP 60

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:11:26 : Search time 51.8018 Seconds
(without alignments)
295.816 Million cell updates/sec

Title: US-09-929-546-8

Perfect score: 619

Sequence: 1 EVLOQSGPELVKPGTGSVRI.....CAAGNFDVWQGGTTLTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_101002.*

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- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	619	100.0	115	19	AAW47084
2	619	100.0	115	21	AAW47084
3	619	100.0	115	22	AAW47084
4	619	100.0	115	23	AAW47084
5	619	100.0	115	24	AAW47084
6	619	100.0	115	25	AAW47084
7	619	100.0	115	26	AAW47084
8	619	100.0	115	27	AAW47084
9	619	100.0	115	28	AAW47084
10	619	100.0	115	29	AAW47084

11	507.5	82.0	118	15	AAW47084	Anti HIV antibody
12	505.5	81.7	137	17	AAW47084	Anti-human gp39 MA
13	502	81.1	109	22	AAW47084	Single-chain antic
14	500.5	80.4	116	19	AAW47084	Anti-Pas MAB chll
15	497.5	80.4	116	21	AAW47084	Anti-Pas MAB chll
16	497.5	80.4	116	21	AAW47084	Anti-human Fas Ig
17	497.5	80.4	118	20	AAW47084	Anti-tissue factor
18	497.5	80.4	118	20	AAW47084	Anti-tissue factor
19	497.5	80.4	130	19	AAW47084	Anti-Pas MAB chll
20	497.5	80.4	135	19	AAW47084	Variable region of
21	497.5	80.4	135	19	AAW47084	Chimeric anti-tiss
22	497.5	80.4	135	19	AAW47084	Chimeric anti-tiss
23	497.5	80.4	500	18	AAW47084	Anti-human Fas mon
24	497.5	80.4	500	19	AAW47084	Anti-human Fas mon
25	496	80.1	136	17	AAW47084	HumC3 VH region BR
26	495.5	80.0	116	19	AAW47084	Variable region of
27	494.5	79.9	120	22	AAW47084	Mouse gungioliside
28	494.5	79.9	139	14	AAW47084	Chimeric 128.1 VH
29	494.5	79.9	139	14	AAW47084	Chimeric 128.1 VH
30	494.5	79.9	139	14	AAW47084	Chimeric 128.1 VH
31	494.5	79.9	139	14	AAW47084	Chimeric 128.1 VH
32	494.5	79.9	139	14	AAW47084	Chimeric 128.1 VH
33	494.5	79.9	235	14	AAW47084	Chimeric 128.1 VH
34	494.5	79.9	235	14	AAW47084	Chimeric 128.1 VH
35	494.5	79.9	235	14	AAW47084	Chimeric 128.1 VH
36	493.5	79.7	232	17	AAW47084	Anti-CD44 heavy cha
37	492.5	79.6	135	20	AAW47084	Anti-CD44 heavy cha
38	492.5	79.6	135	20	AAW47084	Anti-CD44 heavy cha
39	492.5	79.6	135	20	AAW47084	Anti-CD44 heavy cha
40	492	79.5	135	20	AAW47084	Anti-CD44 heavy cha
41	491.5	79.4	135	20	AAW47084	Anti-CD44 heavy cha
42	491.5	79.4	135	20	AAW47084	Anti-CD44 heavy cha
43	491	79.3	121	13	AAW47084	Heavy chain variab
44	490.5	79.2	240	18	AAW47084	Anti-CD44 heavy cha
45	490.5	79.2	434	14	AAW47084	Anti-CD44 heavy cha

ALIGNMENTS

RESULT 1

AAW47084
AD AAW47084 standard; Protein: 115 AA.

XX
AC AAW47084;

DT 26-JUN-1998 (first entry)

DE Mouse J591 monoclonal antibody heavy chain variable region.

XX Mouse: monoclonal antibody; J591; prostate specific membrane antigen;
XX cancer; vascular endothelial cell; metastatic adenocarcinoma.

OS Mus sp.

XX W09803873-Al.

PN 29-JAN-1998.

PT 17-JUL-1997; 97WO-US12035.

XX 09-APR-1997; 97US-083682.

XX 18-JUL-1996; 96US-002125.

XX (CORR) CORNELL RES FOUND INC.

XX Bander NH;

XX WPI; 1998-120937/11.

XX N-PSDB; AAV13950.

XX destroying cancer cells with agent that binds to prostate specific
XX membrane antigen - on vascular endothelial cells near the cancer, or
PT

PT Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
PT or killing cancerous, especially non-prostate, cells (e.g. breast
PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the
PT liver).

XX Example 12; Column 24; 33pp; English.

XX The present invention describes a method of killing cancer cells,
CC particularly prostate cancer cells, by directing a biological agent to
CC the cells which then binds to a prostate specific membrane antigen and
CC which may be bound to a biological agent, the internalisation of the agent,
CC which may be bound to a biological agent, then leads to the death of the cell. The present sequence forms
CC then leads to the death of the cell. The present sequence forms
CC part of an antibody which may be used as the biological agent of the
CC invention. In addition to prostate cancer, the method can be used with
CC renal, urothelial, colon, renal, lung and breast cancer cells, and
CC cancerous cells of metastatic adenocarcinoma to the liver.

XX Sequence 115 AA;
SQ

Query Match 100.0%; Score 619; DB 22; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.2e-47;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFTTHWKQSHGKSLKLEINPNNGTTY 60
XX
DB 1 EVLOQSGPELVKPGTSVRISCKTSGYTFTTHWKQSHGKSLKLEINPNNGTTY 60
XX

OY 61 NQKFEDKATLVVDKSSSTAYMELRSITSDSAVYYCAAGNFDYMGQGTTLTVSS 115
XX
DB 61 NQKFEDKATLVVDKSSSTAYMELRSITSDSAVYYCAAGNFDYMGQGTTLTVSS 115
XX

RESULT 4
AA47083
ID AA47083 standard; Protein, 130 AA.
XX
AC AA47083;
XX
DT 26-JUN-1998 (first entry)
XX
XX Mouse J591 monoclonal antibody heavy chain.
XX
KW Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
KW cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX
OS Mus sp.
XX
XX W09803873-AL.
XX
PD 29-JAN-1998.
XX
PD 17-JUL-1997; 97MO-US12035.
XX
PF 09-APR-1997; 97US-0838682.
XX
PR 18-JUL-1996; 96US-0022125.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Bander NH;
XX
XX WPI; 1998-120937/11.
XX
DR N-PSDB; AAV13949.
XX
XX Destroying cancer cells with agent that binds to prostate specific
XX membrane antigen; cancerous cells near the cancer, or
XX on normal, hypertrophic or cancerous prostatic cells, also used for
XX diagnosis
XX
XX Example 12; Page 53-54; 94pp; English.

XX The present sequence represents the mouse J591 monoclonal antibody heavy
XX chain from an example of the present invention. The present invention
CC

CC describes the elimination of cancer cells by treating vascular
CC endothelial cells (VEC) close to the cancer with an agent (A) able to
CC bind to the extracellular domain (ECD) of prostate specific membrane
CC antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells.
CC (A) is a monoclonal antibody (MAB) that binds to PSMA. The method
CC binding of labelled (A) to VEC close to, or within, a cancer tissue; (2)
CC eliminating or detecting normal, benignly hyperplastic or cancerous
CC prostate epithelial cells using optionally labelled (A); (3) hybridomas
CC that produce a monoclonal antibody (MAB) that binds to PSMA. The method
CC is used to treat renal, urothelial, colon, lung, rectal or breast
CC cancers and metastatic adenocarcinoma of the liver. The diagnostic
CC method of the present invention relates to the detection of prostate disease or
CC the effect of treatments for prostate cancer. The presence of
CC PSMA in the serum indicates that prostate cells are being lysed. (A)
CC binds to an epitope of PSMA expressed on live cells (contrast antibody
CC 7E11 which only binds after cell lysis), allowing targeting of live,
CC unfixed cells and thus providing more efficient treatment and diagnosis.
CC Both cancer cells themselves and the VEC on which they depend are
CC killed. All VEC close to cancer cells express PSMA, whatever the type of
CC cancer, but normal VEC do not.

XX Sequence 130 AA;
SQ

Query Match 100.0%; Score 619; DB 19; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.5e-47;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFTTHWKQSHGKSLKLEINPNNGTTY 60
XX
DB 11 EVLOQSGPELVKPGTSVRISCKTSGYTFTTHWKQSHGKSLKLEINPNNGTTY 70
XX

OY 61 NQKFEDKATLVVDKSSSTAYMELRSITSDSAVYYCAAGNFDYMGQGTTLTVSS 115
XX
DB 71 NQKFEDKATLVVDKSSSTAYMELRSITSDSAVYYCAAGNFDYMGQGTTLTVSS 125
XX

RESULT 5
AA490368
ID AA490368 standard; Protein, 130 AA.
XX
AC AA490368;
XX
XX 15-JAN-2001 (first entry)
XX
XX J591 monoclonal antibody heavy chain protein sequence #2.
DE
XX
KW J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
KW prostate specific membrane antigen; prostate cancer; heavy chain.
XX
XX Homo sapiens.
XX
XX US6107090-A.
XX
PD 22-AUG-2000.
XX
PF 09-APR-1997; 97US-0838682.
XX
XX 06-MAY-1996; 96US-0015976.
XX
XX 18-JUL-1996; 96US-0022125.
XX
XX (CORR) CORNELL RES FOUND INC.
XX
XX Bander NH;
XX
XX WPI; 2000-571325/53.
XX
DR N-PSDB; AAV37831.
XX
XX Antibody specific for extracellular prostate-specific membrane antigen,
XX useful for diagnosis and treatment of prostate cancer
XX
XX Example 12; Fig 7; 33pp; English.

XX This sequence is the heavy chain of the monoclonal antibody J591.

CC The invention relates to an isolated antibody or its antigen binding
 CC portion (i) which binds to an extracellular domain of prostate specific
 CC membrane antigen and which does not require cell lysis to bind to the
 CC antigen, and (ii) which binds to an antigenic epitope of the antigen
 CC selected for its ability to bind to live cells (i) is a fusion protein
 CC comprising a polypeptide chain of the antigenic epitope of the antigen
 CC and a polypeptide chain of a protein which is not involved in the
 CC diagnosis of diseases associated with the presence of normal, benign
 CC hyperplastic, and cancerous epithelial cells or portions. Also it can be
 CC used for identifying the recurrence of such diseases, particularly when
 CC the disease is localised in a particular biological material of the
 CC patient for e.g. recurrence of prostatic disease. They can also be used
 CC for the treatment of a disease, particularly a disease which can be used
 CC to kill cancerous cells or portions of cancerous cells. The invention
 CC relates to a substance effective to kill cancerous prostate
 CC epithelial cells or portions of cancerous cells. The invention
 CC relates to a method of using the antibody with the prostate specific
 CC antigen, permits the therapeutic use of intracellularly acting cytotoxic
 CC agents. (i) targets only prostate epithelial cells and other tissue are
 CC spared which provides safer treatment particularly for elderly patients.
 CC The antibodies bind to living prostate cells and treatments using these
 CC antibodies are more effective than those which target lysed prostate
 CC cells.

XX Sequence 130 AA;

Query Match 100.0%; Score 619; DB 21; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.5e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVLOQSGPELVKPGTGVRIKSTSGYTFETTHVWQSHGKSLKLEWGNINPNNGTGY 60
 Db 11 EVLOQSGPELVKPGTGVRIKSTSGYTFETTHVWQSHGKSLKLEWGNINPNNGTGY 70
 Oy 61 NQKFEKATLVDKSSSTAYMELRSLTSDSAVYCAAGNFDYWGCGTTLTVSS 115
 Db 71 NQKFEKATLVDKSSSTAYMELRSLTSDSAVYCAAGNFDYWGCGTTLTVSS 125

RESULT 6

AAB36219
 ID AAB36219 standard; Protein: 130 AA.

XX AAB36219;

XX 15-FEB-2001 (first entry)

DE Murine heavy chain monoclonal antibody J591 #2.

XX Mouse; antibody; heavy chain; prostate cancer; biological agent.

XX Mus sp.

XX US6136311-A.

XX 24-OCT-2000.

XX 17-JUL-1997; 97US-0895914.

XX 05-MAY-1996; 96US-0016976.

XX 19-APR-1996; 96US-0016976.

XX 01-APR-1997; 97US-0836662.

XX (CORR) CORNELL RES FOUND INC.

XX Bandier NH;

XX WPI: 2001-040234/05.

XX N-PSDB; AAC65538.

XX Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
 XX or killing cancerous, especially non-prostate, cells (e.g. breast
 XX cancerous cells or cancerous cells of metastatic adenocarcinoma to the
 XX liver)

XX Example 12; Fig 7; 35pp; English.

CC The present invention describes a method of killing cancer cells,
 CC particularly prostate cancer cells, by directing a biological agent to
 CC the cells which then binds to a prostate specific membrane antigen and
 CC causes the molecule to be internalised. The internalisation of the agent,
 CC causes the molecule to be internalised. The internalisation of the agent,
 CC then leads to the death of the cell. The present sequence forms
 CC part of an antibody which may be used as the biological agent of the
 CC invention. In addition to prostate cancer, the method can be used with
 CC renal, urothelial, colon, renal, lung and breast cancer cells, and
 CC cancerous cells of metastatic adenocarcinoma to the liver.

XX Sequence 130 AA;

Query Match 100.0%; Score 619; DB 22; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.5e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVLOQSGPELVKPGTGVRIKSTSGYTFETTHVWQSHGKSLKLEWGNINPNNGTGY 60
 Db 11 EVLOQSGPELVKPGTGVRIKSTSGYTFETTHVWQSHGKSLKLEWGNINPNNGTGY 70
 Oy 61 NQKFEKATLVDKSSSTAYMELRSLTSDSAVYCAAGNFDYWGCGTTLTVSS 115
 Db 71 NQKFEKATLVDKSSSTAYMELRSLTSDSAVYCAAGNFDYWGCGTTLTVSS 125

RESULT 7

AAB37085
 ID AAB37085 standard; Protein: 301 AA.

XX AAB37085;

XX 14-JUL-1998 (first entry)

XX Anti-human SC single chain Fv/protamine fusion protein.

XX Fusion protein; SC single chain Fv/protamine fusion protein; SECR;
 XX exogenous gene; serpin enzyme complex receptor; gene therapy;

XX target binding moiety.

XX Homo sapiens.

XX Mus sp.

XX WO9746100-A1.

XX 11-DEC-1997.

XX 03-JUN-1997; 97WO-US09858.

XX 03-JUN-1996; 96US-0656906.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Davis PB, Ferkol TW, Zlady A;

XX WPI: 1998-041783/04.

XX N-PSDB; AAU0611.

XX Delivering compacted exogenous nucleic acid to cells - by targeting
 XX the serpin enzyme complex receptor, used in gene therapy

XX Example 9; Pages 120-121; 158pp; English.

XX This represents an anti-human SC single chain Fv/protamine fusion protein
 XX sequence containing a target binding moiety capable of binding to a moiety.
 XX This can be used in a method for delivering an oligonucleotide to a
 XX mammalian cell. The method comprises conjugating the target binding
 XX moiety to a nucleic acid binding moiety to form a carrier and coupling
 XX the carrier to an expression vector encoding one or more gene products
 XX to form a pharmaceutical composition. A mammalian cell having on its
 XX surface SECR, is contacted with the pharmaceutical composition under the
 XX conditions allowing binding to the receptor resulting in delivery of the

pharmaceutical composition to the interior of the cell. The composition and method are used for the introduction of exogenous genetic material into target host cells expressing SECR on their surface. The nucleic acid may encode a functional wild-type or mutant gene or may be an antisense gene. The nucleic acid may be fused to a protein or may be fused to a protein. The protein may comprise a protein portion having therapeutic properties, e.g. enzymatic activity, cytokine activity and antibiotic activity which is delivered to a cell surface via the SECR binding moiety. The nucleic acid can be compacted at high concentrations with the carrier molecule at a critical salt concentration. The condensations of such complexes provides structural features to the DNA/cationic lipid complex that prolong *in vivo* expression.

Query Match 83.5%; Score 517; DB 19; Length 301;
Best Local Similarity 81.0%; Pred. No. 6.3e-38;
Matches 98; Conservative 8; Mismatches 9; Indels 6; Gaps 1;
QY 1 EVOLQSGPELVKPGTSYVRISCKTSGYTFEYTHHWKSHGSKLEWIGINPNNGSTY 60
DB 127 EVOLQSGPELVKPGTSYVRISCKTSGYTFEYTHHWKSHGSKLEWIGINPNNGSTY 186
QY 61 NQKFDKATLVTKSSYATMELKSLTSDSAVYTCAGWNP-----DTWGQGTTLTV 114
DB 187 NQKFDKATLVTKSSYATMELKSLTSDSAVYTCAGWNP-----DTWGQGTTLTV 246
QY 115 S 115
DB 247 S 247

RESULT 8
AAR12356
XO AAR12356 standard; Protein: 141 AA.
AC AAR12356;
XX

15-AUG-1991 (first entry)

Heavy chain variable region of murine 2G12 immunoglobulin.

Chimeric antibodies; Immunoconjugates; HIV; AIDS.

Mus musculus.

WO9107493-A.

30-MAY-1991.

13-NOV-1990; 50MO-US06615.

13-NOV-1989; 89US-0433730.

(XOMA-) XOMA CORP.

(GRC) GREEN CROSS CORP.

Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;

N-PSDB; AAQ12058.

New chimeric mouse-human antibodies - used to detect, kill and

remove HIV-1 antigen from sample

disclosure; fig 7; 107pp; English.

This is the heavy-chain variable (V) region of a mouse monoclonal antibody (MAb), 2G12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 2G12 since they have an increased compatibility in humans. The heavy and

light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used as immunomodulators. See also AAQ12056-57 and AAQ12059-63.

Query Match 83.4%; Score 516.5; DB 12; Length 141;
Best Local Similarity 80.3%; Pred. No. 3.1e-38;
Matches 98; Conservative 8; Mismatches 9; Indels 7; Gaps 1;
QY 1 EVOLQSGPELVKPGTSYVRISCKTSGYTFEYTHHWKSHGSKLEWIGINPNNGSTY 60
DB 20 EVOLQSGPELVKPGTSYVRISCKTSGYTFEYTHHWKSHGSKLEWIGINPNNGSTY 79
QY 61 NQKFDKATLVTKSSYATMELKSLTSDSAVYTCAGWNP-----DTWGQGTTLTV 113
DB 80 NQKFDKATLVTKSSYATMELKSLTSDSAVYTCAGWNP-----DTWGQGTTLTV 139
QY 114 SS 115
DB 140 SA 141

RESULT 9
AAR12234
XO AAR12234 standard; Protein: 140 AA.
AC AAR12234;
XX

19-AUG-1991 (first entry)

Mouse MAb 2G12 H chain V region.

HIV-1; chimera.

Mus sp.

WO9107494-A.

30-MAY-1991.

13-NOV-1990; 50MO-US06627.

13-NOV-1989; 89US-0433703.

(XOMA-) XOMA CORP.

Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;

N-PSDB; AAQ12014.

New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.

disclosure; Fig 7; 108pp; English.

The mouse VII gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections. and may be produced by a bacterial, yeast or mammalian expression system.

Sequence 140 AA;

Query Match 83.3%; Score 515.5; DB 12; Length 140;
Best Local Similarity 81.0%; Pred. No. 3.7e-38;
Matches 98; Conservative 7; Mismatches 9; Indels 7; Gaps 1;
QY 1 EVOLQSGPELVKPGTSYVRISCKTSGYTFEYTHHWKSHGSKLEWIGINPNNGSTY 60

Db 20 EVOLQSGPELVKPGASVKISKTSYGYTFYTHHWKQSHGKSLWIGINPNNGTTY 79
 Qy 61 NQKPEDKATLVDSKSSATYMWELPSLTSDSAYVYCAQHN-----EDYKSGCTTLTV 113
 Db 80 NQKFDKATLVDSKSSATYMWELPSLTSDSAYVYCAARRNLVYGNFWATYWGSGPLTV 139
 Qy 114 S 114
 Db 140 S 140
 RESULT 10
 AAR55122
 ID AAR55122 standard; Protein; 118 AA.
 AC AAR55122;
 XX 27-JAN-1995 (first entry)
 XX Mouse anti-HIV mu5.5 heavy chain variable region.
 DE
 XX Antibody; heavy chain; anti-HIV antibody; neutralisation;
 KW human immunodeficiency virus; variable region; VH chain; murine.
 XX
 XX Mus musculus.
 FH Key Location/Qualifiers
 FT Region 1..30 /label= FR1
 FT Region 31..35 /label= CDR1
 FT Region 36..49 /label= FR2
 FT Region 50..66 /label= CDR2
 FT Region 67..98 /label= FR3
 FT Region 99..107 /label= FR4
 FT Region 108..118 /label= FR4
 FT Region 109..118 /label= FR4
 FN JP06125793-A.
 XX 10-MAY-1994.
 XX 28-DEC-1991; 91JP-0359809.
 PF 28-DEC-1991; 91JP-0359809.
 PR (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
 PA WPI: 1994-187942/23.
 DR N-PSDB; AAQ65553.
 XX Mouse-human chimeric anti-HIV antibody heavy and light chains -
 PT and recombinant antibody consisting of the H- and L-chains,
 XX useful in AIDS therapy
 XX Example 3; Fig 3; 22pp; Japanese.
 XX Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
 CC The heavy and light chain variable regions from these antibodies
 CC were introduced into human framework regions to construct chimeric
 CC antibodies (AAR55124-R55127).
 CC
 XX Sequence 118 AA:
 Query Match 82.0%; Score 507.5; DB 15; Length 118;
 Best Local Similarity 81.4%; Fred. No. 1.6e-37;
 Matches 96; Conservative 10; Indels 3; Gaps 1;

Qy 1 EVOLQSGPELVKPGASVKISKTSYGYTFYTHHWKQSHGKSLWIGINPNNGTTY 60
 Db 61 NQKPEDKATLVDSKSSATYMWELPSLTSDSAYVYCAQHN-----EDYKSGCTTLTV 113
 Qy 61 NQKPEDKATLVDSKSSATYMWELPSLTSDSAYVYCAQHN-----EDYKSGCTTLTV 113
 Db 61 NQKPEDKATLVDSKSSATYMWELPSLTSDSAYVYCAQHN-----EDYKSGCTTLTV 113
 RESULT 11
 AAR60301
 ID AAR60301 standard; Protein; 118 AA.
 AC AAR60301;
 XX 09-MAR-1995 (first entry)
 XX Anti HIV antibody heavy chain variable region.
 DE
 XX Antibody; heavy chain; light chain; human immunodeficiency virus;
 KW HIV; human immunodeficiency virus; variable region; AIDS; treatment;
 XX prophylaxis; Mus musculus; Homo sapiens.
 XX
 XX Mus musculus.
 FH Key Location/Qualifiers
 FT Region 1..30 /label= Framework region 1.
 FT Region 31..35 /label= CDR1.
 FT Region 36..49 /label= Framework region 2.
 FT Region 50..66 /label= CDR2.
 FT Region 67..98 /label= Framework region 3.
 FT Region 99..107 /label= CDR3.
 FT Region 108..118 /label= Framework region 4.
 FN W09415969-A.
 XX 21-JUL-1994.
 XX 14-JAN-1993; 93WO-JP00039.
 PR 14-JAN-1993; 93AU-0032671.
 PR 14-JAN-1993; 93WO-JP00039.
 PA (KAGA) CUEMO SERO THERAPEUTIC RES INST.
 XX Eda Y, Kinachi K, Maeda H, Oasatomi K, Shioaki K;
 PI Tokiyoshi S;
 XX WPI: 1994-249145/30.
 DR N-PSDB; AAQ70371.
 XX Recombinant chimeric anti HIV antibody - useful for the treatment
 PT and prevention of HIV
 XX Claim 12; Figure 3; 51pp; Japanese.
 XX The recombinant antibody light chain has neutralising activity
 CC against HIV. Chimeric antibodies comprising both mouse and human
 CC sequences are useful in the treatment/prevention of AIDS caused by
 CC HIV.
 XX
 XX Sequence 118 AA:
 Query Match 82.0%; Score 507.5; DB 15; Length 118;
 Best Local Similarity 81.4%; Fred. No. 1.6e-37;
 Matches 96; Conservative 10; Indels 3; Gaps 1;

OY 1 EVLOQSGDELVPGTSYRISCKTSGYTFETVTHWKQSHGKSLKLEMINPNNGTTY 60
 Db 1 EVLOQSGDELVPGTSYRISCKTSGYTFETVTHWKQSHGKSLKLEMINPNNGDTSY 60
 OY 61 NQKFEDKATLVDKSSSTAYMELKSLTSDSVAIVYCA---GNFDFYWGQGTTLTVSS 115
 Db 61 TQKFGKATLVDKSSSTAYMELKSLTSDSVAIVYCAITPYAVADSNGQGTSTVSS 118

RESULT 12

AAU03724
 ID AAU03724 standard; Protein: 137 AA.

XX AAU03724;

DT 02-APR-1997 (first entry)

XX Anti-human gp39 MAb 39-1.7 heavy chain variable region.

DE Heavy chain; variable region; murine; mouse; anti-human; disease;
 KW antibody; gp39-1.7 heavy chain; variable region; murine;
 KW disease; inhibition; B-cell; activation; treatment; disorder;
 KW immune; autoimmune; allergic response; organ rejection; drug;
 KW graft versus host; cell imaging; tumour; targeted; delivery;
 KW targeted.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= sig_peptide

FT Peptide 20..137

FT /label= mat_peptide

FT Misc-difference 46 /note= "corresponding codon TTC"

FT Misc-difference 48 /note= "corresponding codon AAT"

FT Misc-difference 50 /note= "corresponding codon AAC"

FT Misc-difference 52 /note= "corresponding codon GCC"

FT Misc-difference 54 /note= "corresponding codon TCT"

FT Misc-difference 57 /note= "corresponding codon CGC"

FT Misc-difference 59 /note= "corresponding codon ACT"

FT Misc-difference 60 /note= "corresponding codon CCA"

FT Misc-difference 61 /note= "corresponding codon GAG"

FT Misc-difference 63 /note= "corresponding codon AGG"

FT Region 50..54 /note= "complementarity determining region 1"

FT Region 59..85 /note= "complementarity determining region 2"

FT Region 118..126 /note= "complementarity determining region 3"

XX W09623071-A2.

XX 01-AUG-1996.

XX 26-JAN-1996; 96WO-0501119.

XX 26-JAN-1995; 95US-0379057.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Arruffo AA, Bajorath J, Gilliland LK, Gordon ML;

PI Harris LJ, Hollenbaugh D, Sliedak AW;

XX
 DR

WPI: 1996-362694/36.

N-PSDB: AAT35976.

XX Monoclonal antibodies specific for different epitope(s) on human
 PT gp39 used for inhibiting a cell cell adhesion and for the diagnosis
 XX of various disorders, e.g. cancer, psoriasis etc..

PS Claim 95; Fig 7B; 167pp: English.

XX The present sequence is the heavy chain variable region of the
 CC murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) was
 CC a member of the IgG1 subclass. The MAb was produced in a mouse
 CC of 6-8 week old BALB/c mouse with a gp39-CD8
 CC fusion protein, and 3 days later harvesting and fusing spleen and
 CC lymph cells to mouse melanoma cells, to produce an anti-human gp39
 CC MAb producing hybridoma. The MAb may be useful for diagnosing
 CC disease states, inhibiting B-cell activation and for treating
 CC immunological disorders, e.g. autoimmune disorders, allergic
 CC responses, organ rejection and graft versus host disease. The
 CC also inhibits the CD40/gp39 interaction, therefore limiting both
 CC tumour cells and to target therapeutic agents to such cells.
 CC The MAb inhibits the CD40/gp39 interaction, therefore limiting both
 CC prim. and sec. responses to T-cell dependent antigens and Ab prodn.
 CC specific to these antigens. A typical compsn. for intramuscular
 CC injection pref. contains 50 mg of MAb in 1 ml of sterile buffered
 CC water.

XX Sequence 137 AA;

Query Match 81.7%; Score 505.5; DB 17; Length 137;

Best Local Similarity 82.2%; Pred. No. 2.9e-37;

Matches 97; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

OY 1 EVLOQSGDELVPGTSYRISCKTSGYTFETVTHWKQSHGKSLKLEMINPNNGTTY 60

Db 20 EVLOQSGDELVPGTSYRISCKTSGYTFETVTHWKQSHGKSLKLEMINPNNGDTFF 79

OY 61 NQKFEDKATLVDKSSSTAYMELKSLTSDSVAIVYCAAGWN---FDYWGQGTTLTVSS 115

Db 80 NQKFGKATLVDKSSSTAYMELKSLTSDSVAIVYCAAGWTNFDYWGQGTTLTVSS 137

RESULT 13

AAU08980

ID AAU08980 standard; protein: 109 AA.

XX AAU08980;

XX 18-DEC-2001 (first entry)

XX Single-chain antibody scFvA7 heavy chain.

DE Antibody; scFvA7; light chain; angiogenesis; vascularisation;

XX Vascular endothelial; growth factor receptor 2; VEGFR-2; carcinoma.

XX Mus sp.

XX Synthetic.

XX EPI130032-A1.

XX 05-SEP-2001.

XX 28-FEB-2000; 2000EP-0104082.

XX 28-FEB-2000; 2000EP-0104082.

XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX Boeldicke T, Welch H, Tesar M, Yayon A;

XX WPI: 2001-591521/67.

XX

Single-chain antibody that recognizes human vascular endothelial growth factor receptor-2 is useful as a marker for angiogenesis or vascularisation in human tissues and for cell sorting of vascular endothelial cells.

Claim 1: Page 20; 35pp: English.

The invention relates to novel single-chain antibody recognizing human vascular endothelial growth factor receptor-2 (VEGFR-2) comprising a polypeptide having variable heavy (VH) and variable light (VL) domains and human and their allelic variants and mutants. The antibody is useful as an immunohistochemical marker for angiogenesis or vascularisation in a human tissue from cryosection or a growing carcinoma, for vascular and stem cell targeting to a drug or toxin, radionuclide, gene or viral coat protein conjugated to it, for cells expressing human vascular endothelial growth factor receptor-2, their progenitor cells, human haematopoietic stem cells from bone marrow, umbilical cord blood or mobilised peripheral blood on bone surfaces. Recombinant single chain antibodies have many advantages compared to monoclonal antibodies derived from hybridomas. The recombinant antibodies are more easily expressed and prepared in vitro, easily purified from the bacteria periplasm or supernatant without the need for extensive purification. No expensive cell-culture medium and complex laboratory is needed and they are prepared by economical and cheap method. Because of the size they penetrate better into cells and tissue and are better used for in vivo imaging and in vivo diagnostic applications. The single-chain antibodies are easily fused to a drug, toxin, radionuclide, gene or a viral coat protein. The present sequence is the variable heavy chain of antibody scFvA7.

Sequence 109 AA:

Query Match 81.1%; Score 502; DB 22; Length 109;
Best Local Similarity 86.2%; Pred. No. 4.4e-37;
Matches 94; Conservative 8; Mismatches 5; Indels 2; Gaps 2;

Oy 1 EVQLQSGPELVKPTGTSVRSICKTSYTFYETTHVWQSGKSKLEWIGINPNSGTSY 60
Db 1 QVRLQSGPELVKPTGTSVRSICKTSYTFYETTHVWQSGKSKLEWIGINPNSGTSY 60
Oy 61 NQKFDKATLVDKSSSTAYMELRSUTSDSAVYICAG-W-NFYDWQ 107
Db 61 NQKFDKATLVDKSSSTAYMELRSUTSDSAVYICAGLNGMDYWG 109

RESULT 14

ID AAU08979 standard; protein: 110 AA.

AAU08979;

18-DEC-2001 (first entry)

Single-chain antibody scFvA2 heavy chain.

Antibody: scFvA7; light chain; angiogenesis; vascularisation;
Vascular endothelial; growth factor receptor 2; VEGFR-2; carcinoma.
Synthetic.

Mus sp.

EPI130032-A1.

05-SEP-2001.

28-FEB-2000; 2000EP-0104082.

28-FEB-2000; 2000EP-0104082.

(GBF) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX PI
XX PT
XX DR

XX XX

XX XX

XX XX

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XX XX

Boeldicke T, Welch H, Tesar M, Yayon A;
WPT: 2001-591521/67.

Single-chain antibody that recognizes human vascular endothelial growth factor receptor-2 is useful as a marker for angiogenesis or vascularisation in human tissues and for cell sorting of vascular endothelial cells.

Claim 1: Page 20; 35pp: English.

The invention relates to novel single-chain antibody recognizing human vascular endothelial growth factor receptor-2 (VEGFR-2) comprising a polypeptide having variable heavy (VH) and variable light (VL) domains and human and their allelic variants and mutants. The antibody is useful as an immunohistochemical marker for angiogenesis or vascularisation in a human tissue from cryosection or a growing carcinoma, for vascular and stem cell targeting to a drug or toxin, radionuclide, gene or viral coat protein conjugated to it, for cells expressing human vascular endothelial growth factor receptor-2, their progenitor cells, human haematopoietic stem cells from bone marrow, umbilical cord blood or mobilised peripheral blood on their surfaces. Recombinant single chain antibodies have many advantages compared to monoclonal antibodies derived from hybridomas. The recombinant antibodies are more easily expressed and prepared in vitro, easily purified from the bacteria periplasm or supernatant without the need for extensive purification. No expensive cell-culture medium and complex laboratory is needed and they are prepared by economical and cheap method. Because of the size they penetrate better into cells and tissue and are better used for in vivo imaging and in vivo diagnostic applications. The single-chain antibodies are easily fused to a drug, toxin, radionuclide, gene or a viral coat protein. The present sequence is the variable heavy chain of antibody scFvA7.

Sequence 110 AA:

Query Match 80.9%; Score 500.5; DB 22; Length 110;
Best Local Similarity 83.5%; Pred. No. 6.1e-37;
Matches 94; Conservative 6; Mismatches 7; Indels 3; Gaps 1;

Oy 1 EVQLQSGPELVKPTGTSVRSICKTSYTFYETTHVWQSGKSKLEWIGINPNSGTSY 60
Db 1 QVQLQSGPELVKPTGTSVRSICKTSYTFYETTHVWQSGKSKLEWIGINPNSGTSY 60
Oy 61 NQKFDKATLVDKSSSTAYMELRSUTSDSAVYICAGM---NFDYWGQ 107
Db 61 NQKFDKATLVDKSSSTAYMELRSUTSDSAVYICAGYSSSLDTWGQ 110

RESULT 15

AAW71882

AAW71882 standard; Protein: 116 AA.

AAW71882;

18-JAN-1999 (first entry)

Anti-Fas MAb CH11 heavy chain variable region.

Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
autoimmune disease; rheumatoid arthritis; therapy; human; mouse;
antibody engineering.

Mus musculus.

Location/Qualifiers

Key 21.03

Region 71.03

Region 50.66

```

FT      Region      /label= CDR2
FT      99..145
FT      /label= CDR3
PN      EP866131-A2.
XX
XX      23-SEP-1998.
XX
XX      20-MAR-1998; 98EP-0302113.
XX
XX      21-MAR-1997; 97JP-0067938.
XX
XX      (SANY ) SANYO CO LTD.
XX
XX      Haruzama H, Nakahara K, Serizawa N, Takahashi T;
XX      Yonehara S;
XX
XX      WPI: 1998-482965/A2.
XX
XX      Production of anti-Fas protein humanised antibodies - for use in
XX      inducing apoptosis on Fas expressing cells in the treatment of
XX      autoimmune diseases, especially rheumatoid arthritis
XX
XX      Example 4: Page 113; 187pp; English.
XX
XX      This is the amino acid sequence of the heavy chain variable region
XX      (mature protein) of mouse anti-human Fas antigen monoclonal antibody
XX      CH11. The sequence has been compared with an antibody sequence
XX      database, and the framework regions were found to show homology to
XX      the chicken germline antibody sequences. The amino acid sequences
XX      of human HVR5-1 (Genbank: AF013663) and HVR3-1 (Genbank: AF013664)
XX      for use in the amplification of human heavy chain sequences (see
XX      AAV66631). The invention relates to novel humanised antibodies
XX      comprising humanised light and heavy chains (see AAV71876-81) of CH11.
XX      These humanised anti-human Fas antibodies are capable of inducing
XX      apoptosis in cells expressing Fas (e.g. synoviocytes) and are
XX      useful in the treatment of autoimmune disease and chronic
XX      rheumatoid arthritis.
XX
XX      Sequence 116 AA:

Query Match      80.4%; Score 497.5; DB 19; Length 116;
Best Local Similarity 81.9%; Pred. No. 1.2e-36;
Matches 95; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY      1 EVQLQDSGPRLVKCHSVRLSKGSGYTFETVTHWVKOSGKSLKGNINPNNGCTTY 60
      |||||
Db      1 EVQLQDSGPRLVKASVKIKSGAGYTFETDYNHWVKOSGKSLKGNINPNNGCTGY 60

QY      61 NQKFEDKATVTYDKSSSTAYMELRLSTSEDSAVTYCAAG-WNFDYWGQGTTLTVSS 115
      |||||
Db      61 NQKFSKATUTVDNSSSTAYMELRLSTSEDSAVTYCARSTAYMDYWGQGTSTVSS 116

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Job time : 53.8018 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:11:26 ; Search time 48.1982 Seconds
(without alignments)
295.816 Million cell updates/sec

Title: US-09-929-546-19

Perfect score: 569

Sequence: 1 DIVMTQSHKFNSTSGVDRVS.....CQYNSYPLTFGAGTMDLKL 107

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	100.0	107	19	AAW47087
2	569	100.0	107	21	AAW47087
3	528	92.8	108	22	AAW47087
4	528	92.8	108	22	AAW47087
5	526	92.4	115	23	ABW07359
6	524	92.1	223	5	AAAP0031
7	524	92.1	247	9	AAAP0156
8	524	92.1	247	9	AAAP0156
9	521	91.6	107	21	AAW47087
10	513	90.2	107	22	AAW47087

11	507.5	89.2	213	23	AAW2819
12	507.5	89.2	234	23	AAW2819
13	504	88.6	107	15	AAW55121
14	484	88.5	117	15	AAW55121
15	484	88.5	117	15	AAW55121
16	481.5	84.6	106	22	AAW6070
17	481.5	84.6	106	22	AAW6070
18	476	83.7	133	18	AAW21936
19	476	83.7	133	20	AAW21936
20	471	82.8	107	18	AAW01591
21	471	82.8	107	18	AAW01591
22	471	82.8	107	18	AAW01591
23	471	82.8	107	18	AAW01591
24	471	82.8	107	18	AAW01591
25	471	82.8	107	18	AAW01591
26	471	82.8	107	18	AAW01591
27	468	82.2	147	18	AAW19576
28	468	82.2	147	18	AAW19576
29	467	82.1	123	16	AAW6317
30	467	82.1	123	16	AAW6317
31	467	82.1	123	16	AAW6317
32	467	82.1	123	16	AAW6317
33	467	82.1	123	16	AAW6317
34	467	82.1	123	16	AAW6317
35	467	82.1	123	16	AAW6317
36	467	82.1	123	16	AAW6317
37	467	82.1	123	16	AAW6317
38	467	82.1	123	16	AAW6317
39	466	81.9	108	19	AAW48663
40	466	81.9	108	19	AAW48663
41	465.5	81.8	110	17	AAW29999
42	465	81.8	110	17	AAW29999
43	465	81.7	237	20	AAW5440
44	465	81.7	237	20	AAW5440
45	465	81.7	237	20	AAW5440
46	465	81.7	237	20	AAW5440
47	465	81.7	237	20	AAW5440
48	465	81.7	237	20	AAW5440
49	465	81.7	237	20	AAW5440
50	465	81.7	237	20	AAW5440

ALIGNMENTS

RESULT 1
AAW47087
XD AAW47087 standard; Protein; 107 AA.

AC AAW47087;

DT 26-JUN-1998 (first entry)

DE Mouse J591 monoclonal antibody light chain variable region VK17.

DE Mouse: monoclonal antibody: J591; prostate specific membrane antigen;
DE cancer; Vascular endothelial cell, metastatic adenocarcinoma.

OS Mus sp.

PN WO9803873-A1.

XD 29-JAN-1998.

PF 17-JUL-1997; 97MO-US12035.

PR 09-APR-1997; 97US-0838682.

PR 18-JUL-1996; 96US-0022125.

(CORR) CORNELL RES FOUND INC.

Bandier WH;

DR WPI; 1998-120937/11.

DR N-PSDB; AAV13953.

PT Destroying cancer cells with agent that binds to prostate specific
PT membrane antigen - on vascular endothelial cells near the cancer, or

XX Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
 PT or killing cancerous, especially non-prostate, cells (e.g. breast
 PT liver)
 XX
 XX Example 12: Column 26: 35pp; English.
 XX
 XX The present invention describes a method of killing cancer cells,
 CC particularly prostate cancer cells, by directing a biological agent to
 CC the cells which then binds to a prostate specific membrane antigen and
 CC causes the cells to undergo apoptosis. The agent, which is a monoclonal antibody,
 CC which may be bound to a drug or which may act to kill the cells alone,
 CC then leads to the death of the cell. The present sequence forms
 CC part of an antibody which may be used as the biological agent of the
 CC invention. In addition to prostate cancer, the method can be used with
 CC renal, uterine, colon, renal, lung and breast cancer cells, and
 CC cancerous cells of metastatic adenocarcinoma to the liver.
 XX
 XX Sequence 107 AA:
 Query Match 100.04; Score 569; DB 22; Length 107;
 Best Local Similarity 100.04; Pred. No. 3.3e-41;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIVMQSHKFMSTSGVDRVSIITCKASQDVGTAVMYQKQSPKLIYWASTRTGVPD 60
 Db 1 DIVMQSHKFMSTSGVDRVSIITCKASQDVGTAVMYQKQSPKLIYWASTRTGVPD 60
 QY 61 RFTGSGSGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDLKL 107
 Db 61 RFTGSGSGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDLKL 107
 RESULT 4
 ID AAY21817 standard; Protein: 108 AA.
 AC AAY21817;
 XX 10-SEP-1999 (first entry)
 DT Anti-STX1 light chain variable region.
 XX
 XX Humanised; monoclonal antibody; Mab; Shiga toxin; immunoglobulin;
 KW Ig constant region; enterohemorrhagic Escherichia coli; EHEC; uremia;
 KW edema; bloody diarrhoea; hemorrhagic colitis; hemolytic uremic syndrome;
 KW thrombocytopenia; EHEC-mediated disease; anti-STX1.
 XX
 XX Shigella dysenteriae.
 XX
 XX Key Location/Qualifiers
 FT Region 24..34
 FT /note= "complementarity determining region (CDR) 1;
 FT specifically claimed for in claim 10"
 FT Region 50..56
 FT /note= "complementarity determining region (CDR) 2;
 FT specifically claimed for in claim 10"
 FT Region 89..97
 FT /note= "complementarity determining region (CDR) 3;
 FT specifically claimed for in claim 10"
 XX W0932645-A1.
 XX 01-JUL-1999.
 XX 22-DEC-1998; 98WO-0527267.
 XX 18-DEC-1998; 98US-0215163.
 XX 23-DEC-1997; 97US-0068635.
 XX (MELT/) MELTON-CELSA A.
 XX (OBRI/) O'BRIEN A. D.

PA (SCHM/) SCHMITT C K.
 PA (STIN/) STINSON J L.
 PA (WONG/) WONG H.
 PT Melton-Celsa A, O'Brien AD, Schmitt CK, Stinson JL;
 PT Wong H;
 XX WPI: 1999-418935/35.
 XX N-PSDB: AAX82029.
 XX Humanized monoclonal antibodies against Shiga toxins, useful for
 XX protection against enterohemorrhagic Escherichia coli or other Shiga
 XX toxin producing bacteria
 XX Claim 5; Fig 3; 75pp; English.
 XX The invention relates to humanised monoclonal antibodies (MAB) against
 XX Shiga toxins. The humanised MAB that binds to Shiga toxin comprises a
 XX constant and a variable region, where: (a) the constant region contains
 XX a humanised region containing at least one of no-hyper variable region.
 XX variable region containing at least one of no-hyper variable region.
 XX Host cells transfected with vectors encoding a humanised MAB against
 XX Shiga toxin type 2 is useful for treating a patient with an infection
 XX caused by enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin
 XX producing bacteria. The humanised MAB can also be used to reduce illness
 XX caused by EHEC or other Shiga toxin producing bacteria. EHEC are
 XX associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic
 XX colitis), hemolytic uremic syndrome (HUS), and acute renal failure. EHEC
 XX MABs ameliorate edema, thrombocytopenia and uremia associated with EHEC
 XX mediated disease. The present sequence represents an anti-STX1 light
 XX chain variable region.
 XX
 XX Sequence 108 AA:
 Query Match 92.84; Score 528; DB 20; Length 108;
 Best Local Similarity 92.58; Pred. No. 9.9e-38;
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIVMQSHKFMSTSGVDRVSIITCKASQDVGTAVMYQKQSPKLIYWASTRTGVPD 60
 Db 1 DIVMQSHKFMSTSGVDRVSIITCKASQDVGTAVMYQKQSPKLIYWASTRTGVPD 60
 QY 61 RFTGSGSGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDLKL 107
 Db 61 RFTGSGSGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDLKL 107
 RESULT 5
 ID ABB07359 standard; Protein: 115 AA.
 AC ABB07359;
 XX 09-APR-2002 (first entry)
 DT 22A5 IgM light chain variable region.
 XX
 XX Immunoglobulin; Ig; reperfusion; ischaemic injury; pathogenic;
 KW vasotropic; antibody; 22A5; IgM.
 XX
 XX Mus musculus.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 109
 FT /note= "encoded by TGA"
 FT W0200193892-A1.
 XX 13-DEC-2001.
 XX 08-JUN-2001; 2001WO-US18510.
 XX 08-JUN-2000; 2000US-210272P.

XX (BLOO-) CENT BLOOD RES INC.
 XX Carroll WC, Moore PD, Hechtman HB;
 PI WPI: 2002-139643/18.
 DR N-PSDB: ABA94516.
 XX
 XX Treating or preventing immunoglobulin-mediated reperfusion or ischemic
 PT injury resulting from e.g. angioplasty or bypass surgery, by
 PT providing an inhibitor of pathogenic immunoglobulin and ischemic
 PT antigen interaction.
 XX
 XX Claim 50: Page 73-74: 77pp: English.
 XX
 XX The invention provides a method of treating or preventing immunoglobulin-
 CC mediated reperfusion or ischemic injury in a subject. The method involves
 CC administering an inhibitor of an interaction between a pathogenic
 CC antibody and a blood-specific antigen, a component of the
 CC complement pathway. The method also involves providing a component of the
 CC immunoglobulin-mediated reperfusion or ischemic injury. In particular,
 CC injury that results following a naturally occurring episode, a surgical
 CC procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
 CC surgery), or in an injury that occurs in a cardiovascular tissue. The
 CC method is also useful for treating or preventing, in a subject, tissue
 CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.
 CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.
 CC region of 2245 IgM, a pathogenic immunoglobulin.
 XX
 XX Sequence 115 AA:
 Query Match 92.4%; Score 526; DB 23; Length 115;
 Best Local Similarity 92.5%; Pred. NO. 1.6e-37;
 Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IVMTQSHKFNSTSGVDRVSIICKASQDVGTAIVMTQKPSKLLIYWASTRTGTGVPDR 61
 DB 1 IVMTQSHKFNSTSGVDRVSIICKASQDVGTAIVMTQKPSKLLIYWASTRTGTGVPDR 60
 QY 62 FTGSGSGTDFLTITNVQSEDADYFCQOYNSYPLTFGAGTGLDK 107
 DB 61 FTGSGSGTDFLTITNVQSEDADYFCQOYNSYPLTFGAGTGLDK 106

PT antibodies analogous to forms from mammals.
 XX
 XX Disclosure; Fig. 3; 79pp: English.
 XX
 XX The protein is encoded by the mRNA coding sequence of the cDNA fragment
 CC contained within recombinant vector pK17G4. Using the vector this
 CC immunoglobulin is produced readily in pure monoclonal form. Genetic
 CC manipulations can be used to produce chimeras of variants drawing their
 CC homology from species differing from each other. Protein manipulation
 CC is also possible.
 XX
 XX Sequence 223 AA:
 Query Match 92.1%; Score 524; DB 5; Length 223;
 Best Local Similarity 90.7%; Pred. NO. 4.4e-37;
 Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIYMTQSHKFNSTSGVDRVSIICKASQDVGTAIVMTQKPSKLLIYWASTRTGTGVPD 60
 DB 10 DIYMTQSHKFNSTSGVDRVSIICKASQDVGTAIVMTQKPSKLLIYWASTRTGTGVPD 59
 QY 61 RFTGSGSGTDFLTITNVQSEDADYFCQOYNSYPLTFGAGTGLDK 107
 DB 70 RFTGSGSGTDFLTITNVQSEDADYFCQOYNSYPLTFGAGTGLDK 116

RESULT 7
 AAP80155
 ID AAP80155 standard; protein; 247 AA.
 AC AAP80155;
 DT 13-OCT-1990 (first entry)
 XX FRS and CDRs from anti-CEA monoclonal antibody.
 XX
 KW Biosynthetic Antibody Binding site (BABS); variable domain;
 KW anti-CEA monoclonal antibody; ss.
 XX
 OS Synthetic.
 XX WO80809344-A.
 XX
 PD 01-DEC-1988.
 XX
 XX 19-MAY-1988; 88WO-US01737.
 XX
 XX 21-MAY-1987; 87US-0052800.
 XX (CREA-) CREATIVE BIOMOLECULES INC.
 XX Huston JS, Oppermann H;
 XX
 XX WPI: 1988-353928/49.
 XX N-PSDB: AAN80181.
 XX
 XX Recombinant multifunctional protein - having an Ab binding site and a
 PT binding site for biological activity, ion sequestering or binding to a solid
 PT support.
 XX
 XX Disclosure; 15pp: English.
 XX
 XX Multi-functional biosynthetic protein comprising FRS and
 CC CDRs with specificity for a tumour antigen CEA.
 CC See also AAN80171-N80192.
 XX
 XX Sequence 247 AA:
 Query Match 92.1%; Score 524; DB 9; Length 247;
 Best Local Similarity 90.7%; Pred. NO. 4.8e-37;
 Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIYMTQSHKFNSTSGVDRVSIICKASQDVGTAIVMTQKPSKLLIYWASTRTGTGVPD 60

141 DIVMTQSHKFMSTVSGDVRVSTICKASODVGAAIAWYQKQKPSKLLIYWASTRTGVPD 200
 QY 61 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTKLEIK 107
 DB 201 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTKLEIK 247

RESULT 8
 AAF80156 standard; protein; 247 AA.
 AC AAF80156;
 XX 14-NOV-1990 (first entry)
 XX Biosynthetic antibody binding site.
 DE Biosynthetic antibody binding site.
 KW multifunctional protein.
 XX W08809344-A.
 PN 01-DEC-1988.
 XX 19-MAY-1988; 88MO-US01737.
 XX 21-MAY-1987; 87US-0052800.
 PR (CREA-) CREATIVE BIOMOLECULES INC.
 PA Huston JS, Oppermann H;
 XX WPI: 1988-353928/49.
 DR N-PSDB; AAF80182.
 XX Recombinant multifunctional protein - having antibody binding site and a
 PT sequence for biological activity, ion sequestering or binding to a
 PT solid support.
 XX Disclosure; 15pp; English.

The biosynthetic antibody binding site forms part of a recombinant
 CC multifunctional protein which also comprises an effector domain, an AA
 CC sequence capable of sequestering an ion, or a sequence capable of
 CC binding to a solid support. The BABS comprises framework regions in both
 CC VH and LH and CDR1 and CDR3 in VH, and CDR1, CDR2 and CDR3 in VL from an
 CC anti-CEA monoclonal antibody. CDR3 in VH is a CDR2 consensus sequence
 CC found in most immunoglobulin VH regions. The effector protein is an
 CC enzyme toxin receptor, binding site, growth factor, cytokine
 CC oncoferritin, tumour necrosis factor, or a protein which binds to solid
 CC calmodulin or metallothionein. The sequence is able to bind to solid
 CC support is streptavidin or a protein A fragment. The protein may be used
 CC for, eg specific binding assays, affinity purification, biocatalysts, drug
 CC targeting, imaging and immunological treatment of oncogenic and
 CC infectious diseases. The protein offers fewer cleavage sites to
 CC circulating proteolytic enzymes and have improved stability.
 CC The protein is rapidly and efficiently secreted from the body.
 CC They also have reduced immunogenicity.

Sequence 247 AA;
 Query Match 92.1%; Score 524; DB 9; Length 247;
 Best Local Similarity 90.7%; Pred. No. 4.8e-37;
 Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDVRVSTICKASODVGAAIAWYQKQKPSKLLIYWASTRTGVPD 200
 DB 141 DIVMTQSHKFMSTVSGDVRVSTICKASODVGAAIAWYQKQKPSKLLIYWASTRTGVPD 200
 QY 61 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTKLEIK 107
 DB 201 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTKLEIK 247

RESULT 9
 AAY79425 standard; protein; 107 AA.
 AC AAY79425;
 XX 01-AUG-2000 (first entry)
 XX T1e2 receptor antagonist antibody 12H8 light chain variable region.
 DE T1e2 receptor: tyrosine kinase receptor; antagonist;
 KW monoclonal antibody; 12H8; light chain; mouse; angiogenesis;
 KW cancer; diabetic retinopathy; macular degeneration; arthritis;
 KW psoriasis; atherosclerosis; bone marrow; gene therapy; inhibitor;
 KW antipsoriatic; antiarthritic; antiinflammatory; proliferative;
 KW antiatherosclerotic; antianaemic.
 XX W08 musculus.

Key Location/Qualifiers
 PH Region 24..34
 FT /note= *complementarity determining region 1*
 FT Region 50..56
 FT /note= *complementarity determining region 2*
 FT Region 89..97
 FT /note= *complementarity determining region 3*
 XX W0200018437-AL.
 XX 06-APR-2000.
 XX 28-SEP-1999; 99MO-US22421.
 XX 28-SEP-1998; 98US-0102100.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Holmes SD, Erickson-Miller CL, Winkler JD;
 XX WPI: 2000-303392/26.
 DR N-PSDB; AAZ94887.

Novel tie receptor antagonist antibodies inhibits angiogenesis useful
 PT for treating e.g. diabetic retinopathy, cancer or for expanding blood
 PT cells for transplant
 XX Claim 10; Page 35; 42pp; English.
 CC The present sequence is that of the light chain variable region of
 CC murine monoclonal antibody 12H8, as deduced from isolated cDNA
 CC clones (see AA294887). 12H8 is an antagonist antibody of the tie2
 CC receptor; the antibody binds to the tie2 receptor and inhibits
 CC angiogenesis. The tie2 receptor antagonist antibody (which may be
 CC humanized) is useful for inhibiting angiogenesis in a mammal for:
 CC (1) treating an angiogenic disease especially diabetic retinopathy
 CC and cancer; (2) treating psoriasis or atherosclerosis; (3) expansion of
 CC cancer cells transfected with a gene for gene therapy; (4)
 CC expanding cord blood, marrow or peripheral blood cell for
 CC transplant; (5) enhancing the survival of haematopoietic progenitor
 CC cells; and (6) to increase the proliferation of megakaryotic
 CC (progenitor) cells for increasing platelet numbers (all claimed).

Sequence 107 AA;
 Query Match 91.6%; Score 521; DB 21; Length 107;
 Best Local Similarity 90.7%; Pred. No. 3.9e-37;
 Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIVMTQSHKFMSTVSGDVRVSTICKASODVGAAIAWYQKQKPSKLLIYWASTRTGVPD 60

Db. 1 DIVMTGSHKFMSTVSGDVRVSTCKASQDVGVAVMWQKQKPOQSPKLLIYWASSRHTGVPD 60
 Oy 61 RFTGSGSGDTPLTITTVQSEDLADYFCOQYNSYPLTFGAGTMDLX 107
 Db 61 RFTGSGSGDTPLTITTVQSEDLADYFCOQYNSYPLTFGAGTMDLX 107

RESULT 10

AA059665 standard; Protein: 107 AA.
 XX AA059665;
 XX

30-APR-2001 (first entry)

XX Murine Fd138-80 antibody light chain SEQ ID NO: 50.

XX Humanized immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 XX light chain; graft-versus host disease; erythematous; myasthenia gravis;
 XX multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 XX myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
 XX Mus sp.

XX US0180370-B1.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 19-DEC-1989; 89US-0210252.

XX 28-SEP-1989; 89US-0132474.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190855/19.

XX Producing humanized immunoglobulin, involves producing a cell
 XX containing DNA segments encoding humanized heavy and light chain
 XX variable regions, and expressing the DNA segments in the cell -
 XX Example 6; Fig 3; 145pp; English.

XX The present invention describes a method of producing humanised
 XX immunoglobulins involving an immunoglobulin. This is obtained by selecting a
 XX humanised version of an immunoglobulin. This is obtained by selecting a
 XX donor and human immunoglobulin and producing a combined antibody which
 XX contains part of each. These are useful in the treatment of
 XX graft-versus-host disease, transplant rejection, autoimmune diseases such
 XX as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 XX and systemic lupus erythematosus, herpes infections, CMV virus infections
 XX and myeloid leukaemia. The present sequence is an antibody used to
 XX demonstrate the method of the invention.

XX Sequence 107 AA:

Query Match 90.2%; Score 513; DB 22; Length 107;
 Best Local Similarity 90.7%; Pred. No. 1-8e-36;
 Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DIVMTGSHKFMSTVSGDVRVSTCKASQDVGVAVMWQKQKPOQSPKLLIYWASSRHTGVPD 60

Db 1 DIVMTGSHKFMSTVSGDVRVSTCKASQDVGVAVMWQKQKPOQSPKLLIYWASSRHTGVPD 60

Oy 61 RFTGSGSGDTPLTITTVQSEDLADYFCOQYNSYPLTFGAGTMDLX 107

Db 61 RFTGSGSGDTPLTITTVQSEDLADYFCOQYNSYPLTFGAGTMDLX 107

RESULT 11

AAU72819 standard; Protein: 213 AA.
 XX AAU72819;
 XX

26-FEB-2002 (first entry)

XX DNA encoding TRA-8 light chain/human Ig light chain fusion (LM6).

XX Tumour necrosis factor-related apoptosis-inducing ligand receptor;
 XX TRAIL; human disease; systemic lupus erythematosus; Hashimoto's disease;
 XX autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
 XX rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
 XX Addison disease; scleroderma; Goodpasture's syndrome; sterility;
 XX myasthenia gravis; multiple sclerosis; Basodow's disease; diabetes;
 XX allergy; arteriosclerosis; myocarditis; cardiomyopathy;
 XX glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
 XX Mus musculus.
 XX Homo sapiens.

XX WO200183560-A1.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-USI4151.

XX 02-MAY-2000; 2000US-201344P.

XX (UABR-) UAB RES FOUND.

XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;

XX WPI; 2002-049338/06.

XX Novel antibody specific for tumour necrosis factor-related
 XX apoptosis-inducing ligand, useful for inhibiting cell proliferation in
 XX cancer -
 XX Example 26; Page 219-220; 229pp; English.

XX The invention describes a novel antibody which recognizes a tumour
 XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
 XX DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
 XX activity to a cell expressing DR5 in vivo. It is also useful for
 XX preparing a therapeutic for selective apoptosis of abnormal or
 XX dysregulated cells, and for inhibiting cell proliferation in a cell,
 XX preferably human breast, ovary, colon, hematopoietic, prostate,
 XX and other cancer cells. The antibody can be used in combination with
 XX also be administered e.g. paclitaxel, taxol or cycloheximide. The may
 XX antibody is used to treat an autoimmune disease, systemic lupus
 XX erythematosus, Hashimoto's disease, rheumatoid arthritis,
 XX graft-versus-host disease, Sjogren's syndrome, Chron's disease,
 XX pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,
 XX autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple
 XX sclerosis, Basodow's disease, insulin-dependent diabetes mellitus,
 XX rheumatoid arthritis, Sjogren's syndrome, Chron's disease, anaemia,
 XX glomerular nephritis, hypoplastic anaemia, rejection after organopathy,
 XX transplantation, and numerous malignancies of lung, prostate, liver,
 XX ovary, lymphatic or breast tissue. Fusions of the TRA-8 light chain
 XX variable region with the human Ig constant region are shown in
 XX AAU72815-AAU72819 and AAU72810.

XX Sequence 213 AA:

Query Match 89.2%; Score 507.5; DB 23; Length 213;
 Best Local Similarity 90.7%; Pred. No. 1e-35;
 Matches 97; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Oy 1 DIVMTGSHKFMSTVSGDVRVSTCKASQDVGVAVMWQKQKPOQSPKLLIYWASSRHTGVPD 60
 Db 1 DIVMTGSHKFMSTVSGDVRVSTCKASQDVGVAVMWQKQKPOQSPKLLIYWASSRHTGVPD 60

Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIVMTQSHKPNSTSVGDRVSIICKASQDVGTAQVQOKPQSPKLLIYVASTRTHTGVPD 60
 1 DIVMTQSHKPNSTSVGDRVSIICKASQDVGTAQVQOKPQSPKLLIYVASTRTHTGVPD 60
 Db 1 DIVMTQSHKPNSTSVGDRVSIICKASQDVGTAQVQOKPQSPKLLIYVASTRTHTGVPD 60
 OY 61 RFTSGSGDPTLTITINVOSEDLADYFCQOYNSYPLTFGAGTMLDLK 107
 61 RFTSGSGDPTLTITINVOSEDLADYFCQOYNSYPLTFGAGTMLDLK 107
 Db 61 RFTSGSGDPTLTITINVOSEDLADYFCQOYNSYPLTFGAGTMLDLK 107

RESULT 14
 AAR60300
 ID AAR60300 standard; Protein: 107 AA.
 XX AC AAR60300;
 XX AC AAR60300;
 DT 09-MAR-1995 (first entry)
 XX DE Anti HIV antibody light chain variable region.
 XX KW Antibody; heavy chain; light chain; human immunodeficiency virus;
 KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
 KW prophylaxis; Mus musculus; Homo sapiens.
 XX OS Mus musculus.

Key	Location/Qualifiers
EH Region	1..23
FT Region	/label= Framework region 1.
FT Region	24..34
FT Region	/label= CDR1.
FT Region	35..45
FT Region	/label= Framework region 2.
FT Region	50..56
FT Region	/label= CDR2.
FT Region	57..88
FT Region	/label= Framework region 3.
FT Region	89..97
FT Region	/label= CDR3.
FT Region	98..107
FT Region	/label= Framework region 4.
XX PN	W09415969-A.
XX PD	21-JUL-1994.
XX PR	14-JAN-1993; 93WO-JP00039.
XX PR	14-JAN-1993; 93AU-0032671.
XX PR	14-JAN-1993; 93WO-JP00039.
XX PA	(KAGA) CEMO SERO THERAPEUTIC RES INST.
XX PI	Eda Y, Kimachi K, Maeda H, Osatomi K, Shiozaki K;
XX PI	Tokiyoshi S.
XX DR	WPI: 1994-249145/30.
XX DR	N-PSDB: AA070370.
XX XX	Recombinant chimeric anti HIV antibody - useful for the treatment and prevention of HIV
XX XX	Claim 7; Figure 2; 51pp; Japanese.
XX CC	The recombinant antibody light chain has neutralising activity against HIV. Chimeric antibodies comprising both mouse and human sequences are useful in the treatment/prevention of AIDS caused by HIV.
XX XX	Sequence 107 AA;
XX XX	88.6%; Score 504; DB 15; Length 107;

Best Local Similarity 88.8%; Pred. NO. 1..le-35;
 Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIVMTQSHKPNSTSVGDRVSIICKASQDVGTAQVQOKPQSPKLLIYVASTRTHTGVPD 60
 1 DIVMTQSHKPNSTSVGDRVSIICKASQDVGTAQVQOKPQSPKLLIYVASTRTHTGVPD 60
 Db 1 DIVMTQSHKPNSTSVGDRVSIICKASQDVGTAQVQOKPQSPKLLIYVASTRTHTGVPD 60
 OY 61 RFTSGSGDPTLTITINVOSEDLADYFCQOYNSYPLTFGAGTMLDLK 107
 61 RFTSGSGDPTLTITINVOSEDLADYFCQOYNSYPLTFGAGTMLDLK 107
 Db 61 RFTSGSGDPTLTITINVOSEDLADYFCQOYNSYPLTFGAGTMLDLK 107

RESULT 15
 AAB19746
 ID AAB19746 standard; Protein: 112 AA.
 XX AC AAB19746;
 XX AC AAB19746;
 DT 19-FEB-2001 (first entry)
 XX DE Erythropoietin receptor agonist MAB 3G9 VL region.
 XX KW Erythropoietin receptor; agonist; monoclonal antibody; MAB; mouse;
 KW Light chain variable region; antibody engineering; erythropoiesis;
 KW anaemia; cytopenia; acute renal failure; antianaemic; therapy;
 KW Complementarity determining region; CDR.

Key	Location/Qualifiers
EH Region	24..34
FT Region	/label= CDR1
FT Region	50..56
FT Region	/label= CDR2
FT Region	59..91
FT Region	/label= CDR3
XX PN	W0200061637-A1.
XX PD	19-OCT-2000.
XX PR	14-APR-2000; 2000WO-US10284.
XX PR	14-APR-1999; 99US-0129263.
XX PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX PI	Erickson-Miller CL, Holmes SD, Taylor AH, Young PR;
XX PI	WPI: 2000-679469/66.
XX DR	N-PSDB: AAA88853.
XX PT	Novel erythropoietin receptor agonist antibody useful for enhancing erythropoiesis in the treatment of anemia, cytopenia or acute renal failure
XX XX	Claim 6; Page 50; 70pp; English.
XX CC	The present sequence is that of the light chain variable region (VL) of 3G9, a murine monoclonal antibody (MAB) produced by hybridoma cell line 3G9. MAB 3G9 competes with erythropoietin for binding to the erythropoietin receptor (Epor), and is characterised by agonist activity on erythrocyte production. A claimed Epor agonist antibody comprises the 3G9 VL and VH (see AAB19745) regions. MAB 3G9 can also be used in combination with an Epor antagonist antibody to produce a MAB that incorporate 3G9 VH and VL complementarily determining regions within human frameworks. The Epor agonist antibodies are used in a claimed method for enhancing erythropoiesis, for the treatment of anaemia, cytopenia, acute renal failure, and other conditions with depressed erythrocyte production. Agonist antibodies of Epor have the same therapeutic utility as the natural ligand, but with the advantages of easier purification and longer half-life in vivo.

Db 1 DIVMTQSHKFNSTSGVDRVSTICKASQDVGTVAVMYQKPGSKLLIYNASTRTHTGVPD 60
 Qy 61 RFTGSGSGTDFTLTINVSQEDLADYFCQVNSYPLTFGAGTMDLK 107
 Db 61 RFTGSGSGTDFTLTINVSQEDLADYFCQVNSY-RTFGSGTKLEIK 106

RESULT 12

AAU72802
 ID AAU72802 standard; Protein: 234 AA.

XX AAU72802;

DT 26-FEB-2002 (first entry)

DE TRA-8 light chain.

XX Tumour necrosis factor-related apoptosis-inducing ligand receptor:
 KW TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
 KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
 KW Addison disease; scleroderma; Sjogren's syndrome; Chron's disease; anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
 KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; cancer; antibody; chromosome 9p21-22; TRA-8.

XX Mus musculus.

OS WO200183560-A1.

PA 08-NOV-2001.

PD 02-MAY-2001; 2001WO-US14151.

PF 02-MAY-2000; 2000US-201344P.

PR (UABR-) UAB RES FOUND.

XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;

XX WPI: 2002-049338/06.

DR N-PSDB: AA597063.

PA Novel antibody specific for tumour necrosis factor-related
 PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in
 PT cancer.

PS Claim 30; Page 200; 229pp; English.

XX The invention describes a novel antibody which recognizes a tumour
 XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
 XX (TNF receptor DR5, gp22). The antibody has apoptosis-inducing
 XX activity to a cell expressing gp22. The antibody is useful for
 XX preparing a therapeutic for selective apoptosis of abnormal or
 XX dysregulated cells, and for inhibiting cell proliferation in a cell,
 XX preferably a human breast, ovary, colon, haematopoietic, prostate,
 XX lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
 XX also be administered e.g. paclitaxel, taxol or cycloheximide. The
 XX antibody is used to treat an autoimmune disease, systemic lupus
 XX erythematosus, Sjogren's syndrome, Sjogren's syndrome, Chron's disease,
 XX graft-versus-host disease, Addison disease, scleroderma, Goodpasture's syndrome,
 XX autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple
 XX sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,
 XX allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
 XX glomerular nephritis, hypoplastic anaemia, rejection after organ
 XX transplantation, breast cancer, metastasis of lung, prostate, liver,
 XX ovary, lymphatic and haematopoietic tumours, and for preparing antisera for
 XX isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and
 XX AAU72802). TRA-8 are shown in AAU72795 and AAU72800.

XX Sequence 234 AA;

Query Match 89.2%; Score 507.5; DB 23; Length 234;
 -Best Local Similarity 90.7%; Pred. No. 1.1e-35;
 Matches 97; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
 Qy 1 DIVMTQSHKFNSTSGVDRVSTICKASQDVGTVAVMYQKPGSKLLIYNASTRTHTGVPD 60
 Db 22 DIVMTQSHKFNSTSGVDRVSTICKASQDVGTVAVMYQKPGSKLLIYNASTRTHTGVPD 81
 Qy 61 RFTGSGSGTDFTLTINVSQEDLADYFCQVNSYPLTFGAGTMDLK 107
 Db 82 RFTGSGSGTDFTLTINVSQEDLADYFCQVNSY-RTFGSGTKLEIK 127

RESULT 13

AAU55121

ID AAR55121 standard; Protein: 107 AA.

XX AAR55121;

AC AAR55121;

DT 27-JAN-1995 (first entry)

XX Mouse anti-HIV mu39.1 light chain variable region.

XX Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
 KW human immunodeficiency virus; variable region; VH chain; murine.

XX Mus musculus.

XX Key Location/Qualifiers

XX Region 1..23

FT Region /label= FR1

FT Region 24..34

FT Region /label= CDR1

FT Region 35..49

FT Region /label= FR2

FT Region 50..56

FT Region /label= CDR2

FT Region 57..88

FT Region /label= FR3

FT Region 89..97

FT Region /label= CDR3

FT Region 98..107

FT Region /label= FR4

XX JP06125783-A.

XX 10-MAY-1994.

XX 28-DEC-1991; 91JP-0359808.

XX (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.

XX WPI: 1994-187342/23.

XX N-PSDB: AAQ65552.

XX Mouse-human chimeric anti-HIV antibody heavy and light chains -
 PT and recombinant antibody consisting of the H- and L-chains,
 PT useful in AIDS therapy

XX Example 3; Fig 2; 22pp; Japanese.

XX Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
 CC The heavy and light chain variable regions from these antibodies
 CC were sequenced (AAR55120-R55123). The murine anti-HIV CD8s were
 CC introduced into human framework regions to construct chimeric
 CC antibodies (AAR55124-R55127).

XX Sequence 107 AA;

Query Match 88.6%; Score 504; DB 15; Length 107;
 Best Local Similarity 88.8%; Pred. No. 1.1e-35;

```
SQ Sequence 112 AA;
Query Match      84.7%: Score 482; DB 21; Length 112;
Seq. Id. Similarity 86.0%: Pred. No. 8.2e-34;
Matches 92; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
OY 1 DIVMTQSHKFNSTSVGDRVSIICKASQDVGTAVDWYQOKPGQSPKLLIYWASTHTGTGVPD 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 DIVMTQSQKFNSTSVGDRSVTCKASQNGVGNVARYQOKPGQSPKALISASRYSGVPD 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 RFTGSGSGTDFTLTITNWQSEDLADYFCQYNSYPLPFGAGTMDLK 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 RFTGSGSGTDFTLTISWQSEDLAEYFCQYNSYPLPFGAGTMDLK 107
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Search completed: July 21, 2003, 13:31:21
Job time : 49.1982 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2003, 13:20:30 ; search time 12.4324 seconds
(without alignments)
272.162 Million cell updates/sec

Title: US-09-929-546-8

Perfect score: 619

Sequence: 1 EVOLQSSPELVKSGTSVRI.....CAAGNFYWGQGTTLTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.AA.*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/6C.COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfilled.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	619	100.0	115	3	US-08-838-682-8
2	619	100.0	115	4	US-08-995-914-8
3	619	100.0	115	4	US-09-357-710A-8
4	619	100.0	115	4	US-08-995-914-4
5	619	100.0	130	4	US-08-995-914-4
6	619	100.0	130	4	US-09-357-710A-4
7	517	83.5	301	2	US-08-656-906-25
8	517	83.5	301	4	US-09-217-847-25
9	507.5	82.0	118	1	US-08-491-845-6
10	499.5	80.7	128	1	US-08-202-047-21
11	499.5	80.7	128	3	US-08-464-644-19
12	496	80.1	136	4	US-08-525-539A-47
13	496	80.1	136	4	US-08-116-778B-1
14	494.5	79.9	139	2	US-08-438-562-1
15	494.5	79.9	139	2	US-08-483-528B-91
16	494.5	79.9	139	2	US-08-444-644-33
17	494.5	79.9	233	3	US-08-232-246A-33
18	494.5	79.9	233	4	US-08-232-246A-33
19	494.5	79.9	233	4	US-08-444-644-19
20	494.5	79.9	233	3	US-08-444-644-42
21	494.5	79.9	233	3	US-08-232-246A-19
22	494.5	79.9	235	4	US-08-232-246A-28
23	494.5	79.9	235	4	US-08-232-246A-42
24	494.5	79.9	235	4	US-08-425-763-2
25	493.5	79.7	232	1	US-08-811-757-2
26	493.5	79.7	232	4	US-09-249-230-2
27	493.5	79.7	232	4	US-09-249-230-2

28	492.5	79.6	116	1	US-07-634-278-56
29	492.5	79.6	116	1	US-08-477-728-56
30	492.5	79.6	116	1	US-08-474-040-56
31	492.5	79.6	116	1	US-08-484-537-56
32	492.5	79.6	116	4	US-08-484-537-56
33	492.5	79.6	135	1	US-07-634-278-69
34	492.5	79.6	135	1	US-08-477-728-69
35	492.5	79.6	135	1	US-08-474-040-69
36	492.5	79.6	135	1	US-08-484-537-69
37	492.5	79.6	135	4	US-08-484-537-69
38	491.5	79.4	472	4	US-08-301-593-30
39	491.5	79.4	472	4	US-08-301-593-30
40	491.5	79.3	125	4	US-08-357-710A-20
41	490.5	79.2	454	2	US-07-934-373C-22
42	490.5	79.2	454	3	US-08-437-642B-22
43	490.5	79.2	454	4	US-08-146-206C-22
44	490.5	79.2	454	5	US-08-146-206C-22
45	489.5	79.1	135	1	US-08-137-117D-27

ALIGNMENTS

RESULT 1
US-08-838-682-8
; Sequence 8, Application US/08838682
; Patent No. 6107090
; GENINFORMATION:
; APPLICANT: BANDER M.D., NEIL H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; NUMBER OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; CLAYTON: CLINTON SQUARE, P.O. BOX 1051
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; SOFTWARE: SYMBIOSIS/MS-DOS
; SOFTWARE: SYMBIOSIS/MS-DOS
; CURRENT APPLICATION DATA: Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/838.682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: US 60/016,976
; APPLICATION NUMBER: 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCID NUMBER: 19603/1172
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-682-8

Query Match 100.0%; Score 619; DB 3; Length 115;
Best Local Similarity 100.0%; Pred.No.1.1e-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-682-4

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKFGTSVRISCKTSGYTFETTHWKQSHGKSLWGNINPNNGTTY 60
DB 11 EVLOQSGPELVKFGTSVRISCKTSGYTFETTHWKQSHGKSLWGNINPNNGTTY 70
QY 61 NQKFEDKATLTVDKSSSTAYMELRSLTSDSAVYTCAGWPNFYWGQGTTLTVSS 115
DB 71 NQKFEDKATLTVDKSSSTAYMELRSLTSDSAVYTCAGWPNFYWGQGTTLTVSS 125

RESULT 5
US-08-895-914-4
Sequence 25, Application US/08895914

PATENT NO. 6136311
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603-1051
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: STRIP/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895-914
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 50/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,682
FILING DATE: 09-APR-1997
ATTORNEY/AGENT:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 19603/1173
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-895-914-4

Query Match 100.0%; Score 619; DB 4; Length 130;

Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLOQSGPELVKFGTSVRISCKTSGYTFETTHWKQSHGKSLWGNINPNNGTTY 60
DB 11 EVLOQSGPELVKFGTSVRISCKTSGYTFETTHWKQSHGKSLWGNINPNNGTTY 70
QY 61 NQKFEDKATLTVDKSSSTAYMELRSLTSDSAVYTCAGWPNFYWGQGTTLTVSS 115
DB 71 NQKFEDKATLTVDKSSSTAYMELRSLTSDSAVYTCAGWPNFYWGQGTTLTVSS 125

RESULT 6
US-09-357-710A-4
Sequence 4, Application US/09357710A

PATENT NO. 6290956
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION NUMBER: US/09/357,710A
FILING DATE: 06-MAY-1996
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 130
TYPE: PRT
ORGANISM: Mus sp.
US-09-357-710A-4

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKFGTSVRISCKTSGYTFETTHWKQSHGKSLWGNINPNNGTTY 60
DB 11 EVLOQSGPELVKFGTSVRISCKTSGYTFETTHWKQSHGKSLWGNINPNNGTTY 70
QY 61 NQKFEDKATLTVDKSSSTAYMELRSLTSDSAVYTCAGWPNFYWGQGTTLTVSS 115
DB 71 NQKFEDKATLTVDKSSSTAYMELRSLTSDSAVYTCAGWPNFYWGQGTTLTVSS 125

RESULT 7
US-08-656-906-25
Sequence 25, Application US/08656906

PATENT NO. 5972901
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W.
APPLICANT: Davis, Pamela B.
APPLICANT: Zlady, Assem-Galal
APPLICANT: Serpin Enzyme Complex Receptor -
TITLE OF INVENTION: Isolated Gene Transfer
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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1 APPLICATION NUMBER: US/08/656,906
2 FILING DATE: 03-JUN-1996
3 CLASSIFICATION: 514
4 PRIOR APPLICATION DATA:
5 FILING DATE: 03-JUN-1996
6 PRIORITY DATA: WO 95/25809
7 APPLICATION NUMBER: WO 95/25809
8 FILING DATE: 23-MAR-1995
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 08/216,534
11 FILING DATE: 23-MAR-1994
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Ingolia, Diane E.
14 ADDRESS: 100 NUMBER 40, 027
15 REFERENCE INFORMATION:
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (415) 705-8410
18 TELEFAX: (415) 397-8338
19 INFORMATION FOR SEQ ID NO: 25:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 301 amino acids
22 TYPE: amino acid
23 TOPOLOGY: linear
24 MOLECULE TYPE: Protein
25 US-08-656-906-25
26
27 Query Match 83.5% Score 517
28 Best Local Similarity 81.0% Pred. No.
29 Matches 98: Conservative 8: Mismatch
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31 Oy 1 EVQLQGGPGYVKGGYSRVSKSGSYGFRF
32 Db 127 EVQLQGGPGYVKGGASVSKISCTSGYFR
33
34 Oy 61 NQKFEKATVTVDKSSSTAFYMELRSLTSE
35 Db 187 NQKFGKATVTVDKSSSTAFYMELRSLTSE
36
37 Oy 115 S 115
38 Db 247 S 247
39
40 RESULT 8
41 US-09-217-847-25
42 PRIORITY DATA: Application US/09/217847
43 Patent No. 6200801
44 GENERAL INFORMATION:
45 APPLICANT: Perkol Jr., Thomas W.
46 APPLICANT: Davis, Pamela B.
47 APPLICANT: Zisdy, Assem-Galal
48 TITLE OF INVENTION: Serpin Enzyme Com
49 TITLE OF INVENTION: Mediated Gene Tran
50 CORRESPONDENCE ADDRESS: 51
51 ADDRESSSEE: Medlen & Carroll
52 STREET: 220 Montgomery Street, Suite
53 CITY: San Francisco
54 STATE: California
55 COUNTRY: United States of America
56 MAILING ADDRESS:
57 COMPUTER FILE NO.:
58 MEDIUM TYPE: Floppy disk
59 OPERATING SYSTEM: PC-DOS/MS-DOS
60 SOFTWARE: Patent In Release 1.0, Ver
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/09/217,847
63 CLASSIFICATION:
64 PRIOR APPLICATION DATA:
65 APPLICATION NUMBER: 08/656,906

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1 PILING DATE:
2 PRIOR APPLICATION DATA:
3 PRIOR APPLICATION NUMBER: WO 95/25809
4 PILING DATE: 23-MAR-1995
5 PRIOR APPLICATION DATA:
6 PRIOR APPLICATION NUMBER: US 08/216,534
7 PILING DATE: 23-MAR-1994
8 ATTORNEY/AGENT INFORMATION:
9 NAME:
10 REGISTRATION NUMBER: 40,027
11 REFERENCE/DOCKET NUMBER: CASE-02280
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (415) 705-8410
14 TELEFAX: (415) 397-8338
15 INFORMATION FOR SEQ ID NO: 25:
16 SEQUENCE CHARACTERISTICS:
17 Length: 1000 nucleotides
18 TYPE: amino acid
19 TOPOLOGY: linear
20 MOLECULE TYPE: protein
21 US-09-217-847-25
22
23 Query Match Similarity 83.5% Score 517: DB
24 Best Local Similarity 81.0% Pred. No. 3:dc
25 Matches 98 Conservative 6; Mismatches
26
27 OY 1 EVOLQGSGPLVKGRTGTVNRVSKCKTSKGVTEFTYIT
28 DB 127 EVOLQGSGPLVKGRTGTVNRVSKCKTSKGVTEFTYIT
29 OY 61 NQKFEKATLTVDKSSSTAYMEHLSLTSDSASVY
30 DB 187 NQKFGKATLTVDKSSSTAYMEHLSLTSDSASVY
31 OY 115 S 115
32 DB 247 S 247
33
34 RESULT 9
35 US-08-491-845-6
36 : Sequence 6: Application US/08491845
37 : Patent No. 5773247
38 : GENERAL INFORMATION:
39 : APPLICANT: MAEDA, Hiroaki
40 : APPLICANT: KIMACHI, Kazuhiko
41 : APPLICANT: EDA, Tasuyuki
42 : APPLICANT: SUGIMOTO, Kojirochi
43 : APPLICANT: TOKUYOSHI, Naohiko
44 : APPLICANT: TOKUYOSHI, Naohiko
45 : TITLE OF INVENTION: RECOMBINANT ANTI-HIV AL
46 : TITLE OF INVENTION: PROCESS FOR PREPARING
47 : NUMBER OF SEQUENCES: 17
48 : CORRESPONDENCE ADDRESS:
49 : ADDRESSEE: Broadway and Naimark
50 : CITY: Washington
51 : STATE: D.C.
52 : COUNTRY: USA
53 : ZIP: 20004
54 : COMPUTER READABLE FORM:
55 : MEDIUM TYPE: Floppy disk
56 : COMPUTER: IBM PC compatible
57 : SOFTWARE: SYNGEN, GENES-DO
58 : SOFTWARE: PALIGN, Release 11.0, Version
59 : CURRENT APPLICATION DATA:
60 : APPLICATION NUMBER: US/08/491,845
61 : PILING DATE:
62 : CLASSIFICATION: 435
63 : PRIOR APPLICATION DATA:
64 : APPLICATION NUMBER: PCT/JP93/00039
65 : PILING DATE: NOVEMBER-1991
66 : ATTORNEY/AGENT INFORMATION:

```


RESULT 13
US-08-525-539A-47
: Sequence 47, Application US/08525539A
: Patent No. 6309636
: GENERAL INFORMATION:
: APPLICANT: DE COUTO, FERNANDO J. R.
: APPLICANT: BELLOTTI, ROBERTO L.
: ATTORNEY: PETERSON, JERRY A.
: TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
: TITLE OF INVENTION: MC3 ANTI-BAB46 ANTIBODY, METHODS OF USE THEREOF, AND
: TITLE OF INVENTION: MC3 ANTI-BAB46 ANTIBODY, METHODS OF USE THEREOF, AND
: NUMBER OF SEQUENCES: 81
: CORRESPONDENCE:
: ADDRESSEE: MORRISON & FOERSTER

CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0. Version #1.30
CURRENT APPLICATION DATA: US/08/525.539A
APPLICATION NUMBER: US/08/525.539A
PUBLICATION: 44-ESP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 37,612
 REFERENCE/CKET NUMBER: 27633-20001.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 136 amino acids
 PRESEDING AMINO ACIDS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-525-539A-47

[illegible]

Sequence 1, Application 05708116778E
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CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/116,778
 FILING DATE: 07-SEP-93
 CLASSIFICATION: 424
 NAME: WILSON, MARY J.
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 424
 TELEPHONE: (703)816-4000
 TELEFAX: (703)816-4100
 REFERENCE/DOCKET NUMBER: 249-59
 TELECOMMUNICATION INFORMATION:
 NAME/KEY: domain
 LOCATION: 31..35
 IDENTIFICATION METHOD: BY SIMILARITY
 IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
 OTHER INFORMATION: /product- "HYPERVARIABLE REGION 1"
 FEATURE:
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 LOCATION: 50..66
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 Best Local Similarity 79.24; Pred. No. 2.1e-41;
 Matches 95; Conservative 13; Indels 5; Gaps 1;
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 20 EVLQQGSELVLPKPTSVRIKSTKSTQYTFETTHVWQSHGKSLKLEWGNINPANGTTY 79
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 US-08-438-562-1
 : Sequence 1, Application US/08438562
 : Patent No. 5874255
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, KAZUYASU
 APPLICANT: KOIKE, MASAMICHI
 APPLICANT: SHITARA, KENYA
 APPLICANT: HANAI, NOBUO
 APPLICANT: KUNANA, YOSHITISA
 APPLICANT: HASEGAWA, MAMORU
 NUMBER OF SEQUENCES: 49
 NUMBER OF SEQUENCES ON HUMANIZED ANTIBODIES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,562
 FILING DATE: 07-SEP-93
 CLASSIFICATION: 424
 NAME: WILSON, MARY J.
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 424
 TELEPHONE: (703)816-4000
 TELEFAX: (703)816-4100
 REFERENCE/DOCKET NUMBER: 249-76
 TELECOMMUNICATION INFORMATION:
 NAME/KEY: domain
 LOCATION: 31..35
 IDENTIFICATION METHOD: BY SIMILARITY
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 FEATURE:
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 LOCATION: 50..66
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 US-08-438-562-1
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 Best Local Similarity 79.24; Pred. No. 2.1e-41;
 Matches 95; Conservative 13; Indels 5; Gaps 1;
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 20 EVLQQGSELVLPKPTSVRIKSTKSTQYTFETTHVWQSHGKSLKLEWGNINPANGTTY 79
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 RESULT 15
 US-08-438-562-1
 : Sequence 1, Application US/08438562
 : Patent No. 5874255
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, KAZUYASU
 APPLICANT: KOIKE, MASAMICHI
 APPLICANT: SHITARA, KENYA
 APPLICANT: HANAI, NOBUO
 APPLICANT: KUNANA, YOSHITISA
 APPLICANT: HASEGAWA, MAMORU
 NUMBER OF SEQUENCES: 49
 NUMBER OF SEQUENCES ON HUMANIZED ANTIBODIES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,562
 FILING DATE: 07-SEP-93
 CLASSIFICATION: 424
 NAME: WILSON, MARY J.
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 424
 TELEPHONE: (703)816-4000
 TELEFAX: (703)816-4100
 REFERENCE/DOCKET NUMBER: 249-76
 TELECOMMUNICATION INFORMATION:
 NAME/KEY: domain
 LOCATION: 31..35
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 OTHER INFORMATION: /product- "HYPERVARIABLE REGION 1"
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 FEATURE:
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 LOCATION: 99..109
 IDENTIFICATION METHOD: BY SIMILARITY
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 OTHER INFORMATION: /product- "HYPERVARIABLE REGION 3"
 US-08-438-562-1
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 Best Local Similarity 79.24; Pred. No. 2.1e-41;
 Matches 95; Conservative 13; Indels 5; Gaps 1;
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 QY 61 NQKFDKATLVDKSSSTAYMELKSTSDSAVYICAA-----GNFDMWQSGTTLVWS 115
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 RESULT 15
 US-08-438-562-1
 : Sequence 1, Application US/08438562
 : Patent No. 5874255
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, KAZUYASU
 APPLICANT: KOIKE, MASAMICHI
 APPLICANT: SHITARA, KENYA
 APPLICANT: HANAI, NOBUO
 APPLICANT: KUNANA, YOSHITISA
 APPLICANT: HASEGAWA, MAMORU
 NUMBER OF SEQUENCES: 49
 NUMBER OF SEQUENCES ON HUMANIZED ANTIBODIES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,562
 FILING DATE: 07-SEP-93
 CLASSIFICATION: 424
 NAME: WILSON, MARY J.
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 424
 TELEPHONE: (703)816-4000
 TELEFAX: (703)816-4100
 REFERENCE/DOCKET NUMBER: 249-76
 TELECOMMUNICATION INFORMATION:
 NAME/KEY: domain
 LOCATION: 31..35
 IDENTIFICATION METHOD: BY SIMILARITY
 IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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 IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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 NAME/KEY: domain
 LOCATION: 99..109
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 IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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 US-08-438-562-1
 Query Match 79.94; Score 494.5; DB 2; Length 139;
 Best Local Similarity 79.24; Pred. No. 2.1e-41;
 Matches 95; Conservative 13; Indels 5; Gaps 1;
 QY 1 EVLQQGSELVLPKPTSVRIKSTKSTQYTFETTHVWQSHGKSLKLEWGNINPANGTTY 60
 20 EVLQQGSELVLPKPTSVRIKSTKSTQYTFETTHVWQSHGKSLKLEWGNINPANGTTY 79
 QY 61 NQKFDKATLVDKSSSTAYMELKSTSDSAVYICAA-----GNFDMWQSGTTLVWS 115
 80 NQKFDKATLVDKSSSTAYMELKSTSDSAVYICATYGHYGYMEATWQSGTTLVWSA 139
 DB 80 NQKFDKATLVDKSSSTAYMELKSTSDSAVYICATYGHYGYMEATWQSGTTLVWSA 139
 RESULT 15
 US-08-438-562-1
 : Sequence 1, Application US/08

RESULT 15

US-08-438-562-1	Query Match	79.94	Score	494.5	DB	2	Length	139
: Sequence 1, Application US/08438562	Best Local Similarity	79.24	Pred. No.	2.1e-41				
: Patent No. 5874255	Matches	95	Conservative	7	Mismatches	13	Indels	5
: GENERAL INFORMATION:								

Qy 1 EVQLQSGPELVKPGTSTSRVSRICKSGYPTFTPIHWKQSHGSKSLIEWIGINPNNGTTY 60
Db 20 EVQLQSGPELVKPGKASVYKISKASGYTFTDINQWQKSHGSKSLIEWIGIYPNNGCTY 79
Qy 61 NQKFDKRLATLVKSSSTAYMELASLTSDSAYVYCAA-----GNFDYWGQGLTLYVSS 115
Db 80 NQKFSKRLATLVKSSSTAYMELHSLTSDSAYVYCATYGHVGYMFAFGQGLTVSA 139

Search completed: July 21, 2003, 13:32:25
Job time : 13.4324 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2003, 13:20:30 : Search time 11.5676 Seconds
(Without alignments)
272.162 Million cell updates/sec

Title: US-09-929-546-19
Perfect score: 569
Sequence: 1 DIVVQSHKFMSTVGDRVS.....CQQNSVPLTFGACTMLDLK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_5/ptodata/1/laa/5B.COMB.pep.*
- 3: /cgn2_5/ptodata/1/laa/6A.COMB.pep.*
- 4: /cgn2_5/ptodata/1/laa/6B.COMB.pep.*
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- 6: /cgn2_5/ptodata/1/laa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	569	100.0	107	4	US-08-995-914-19
3	569	100.0	107	4	US-09-357-710A-19
4	513	90.2	107	1	US-07-634-278-50
5	513	90.2	107	1	US-08-477-728-50
6	513	90.2	107	1	US-08-474-040-50
7	513	90.2	107	1	US-08-487-200-50
8	513	90.2	107	4	US-08-484-537-50
9	504	88.6	107	1	US-08-491-845-4
10	490	86.6	107	2	US-08-797-689-18
11	471	83.9	149	2	US-08-646-265A-27
12	471	82.8	127	4	US-08-653-402B-4
13	468	82.2	147	2	US-08-398-613A-20
14	467	82.1	123	1	US-08-398-612A-20
15	467	82.1	123	1	US-08-398-611A-20
16	467	82.1	123	1	US-08-491-334A-20
17	467	82.1	123	3	US-09-027-449-17
18	467	82.1	123	3	US-09-026-985-17
19	467	82.1	123	4	US-09-121-952A-17
20	467	82.1	123	4	US-09-234-340A-17
21	467	82.1	123	4	US-08-752-693A-1
22	466	81.9	108	4	US-08-253-877C-55
23	466	81.9	132	1	US-08-452-164A-55
24	466	81.9	132	2	US-08-976-183A-36
25	466	81.9	132	4	Sequence 19, Appl
26	466	81.9	132	4	Sequence 19, Appl
27	466	81.9	132	4	Sequence 19, Appl

Sequence 37, Appl
Sequence 23, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 5, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-938-682-19
Sequence 19, Application US/08838682
Patent No. 6,822,199
GENERAL INFORMATION:
APPLICANT: Bander M.D., Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
ATTORNEY: Clinton Square, P.O. Box 1051
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603-1051
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: SYBASE, DOS/MS-DOS
SOFTWARE: PATLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,682
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1172
REFERENCE/DOCKET NUMBER: 19603/1172
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: Protein
US-08-938-682-19

Query Match 100.0%; Score 569; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQOYNSYPLTFCAGTMDLX 107

RESULT 2
US-08-855-914-19
; Sequence 19, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CONTACT ADDRESS:
; ADDRESSEE: Milton S. Grange, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM: disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 1997-04-09/06/015,976
; PRIOR APPLICATION NUMBER: US/08/895,914
; PRIOR FILING DATE: 1996-05-06
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 05-MAY-1996
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 1997-07-20
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,682
; FILING DATE: 1997-04-09/06/015,976
; TELEPHONE: (716) 243-6304
; TELEFAX: (716) 243-6304
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-855-914-19

Query Match 100.0%; Score 569; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIVMTGSHKFMSTVGDWRVSIICKASQDVCTAVDMYQKQPSKLLITWASTRHFGVDP 60
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RESULT 3

US-09-357-710A-19
; Sequence 19, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch; B2L 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09/06/015,976
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-19

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Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-406-535-4
; Sequence 4, Application US/09406535
; Patent No. 6376653
; GENERAL INFORMATION:
; APPLICANT: Jonathan D. Hedges
; APPLICANT: Stephen D. Hedges
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: Tie2 Antagonist Antibodies
; FILE REFERENCE: P50844
; CURRENT APPLICATION NUMBER: US/09/406,535
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 60/102,100
; PUBLICATION NUMBER: US 60/102,100
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-406-535-4

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Best Local Similarity 90.7%; Pred. No. 1.1e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Db 1 DIVMTGSHKFMSTVGDWRVSIICKASQDVCTAVDMYQKQPSKLLITWASTRHFGVDP 60
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RESULT 5
US-07-634-278-50

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; Sequence 50, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourie and Crew
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-2400
; TELEFAX: (415) 325-4222
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULES TYPE: peptide
US-07-634-278-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVTQSHKFNSTGVDNRVSIITCKASQDVGVAVDWYQKPGSQSKLLIYWASTRHFGVDP 60
DB 1 DIVTQSHFNSTGVDNRVSIITCKASQDVGVAVDWYQKPGSQSKLLIYWASTRHFGVDP 60

QY 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107
DB 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107

RESULT 7
US-08-474-040-50
; Sequence 50, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourie and Crew
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-2400
; TELEFAX: (415) 325-4222
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULES TYPE: peptide
US-08-477-728-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVTQSHKFNSTGVDNRVSIITCKASQDVGVAVDWYQKPGSQSKLLIYWASTRHFGVDP 60
DB 1 DIVTQSHFNSTGVDNRVSIITCKASQDVGVAVDWYQKPGSQSKLLIYWASTRHFGVDP 60

QY 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107
DB 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107

RESULT 6
US-08-477-728-50
; Sequence 50, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
```

ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
PRIORITY NUMBER: US/08/474,040
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 50:
LENGTH: 107 amino acids
STRANDEDNESS: single
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DIVMTQSHKFMSTVGVDRVSIICKASQDVGAVDMYQKQSQPKLLIYMASTRHRTGVPD 60
DB 1 DIVMTQSHKFMSTVGVDRVSIICKASQDVGAVDMYQKQSQPKLLIYMASTRHRTGVPD 60
Oy 61 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTRLEK 107
DB 61 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTRLEK 107

RESULT 8
US-08-487-200-50
Sequence 50, Application US/08/487200
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
PRIORITY NUMBER: US/08/487,200
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 50:

LENGTH: 107 amino acids
STRANDEDNESS: single
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DIVMTQSHKFMSTVGVDRVSIICKASQDVGAVDMYQKQSQPKLLIYMASTRHRTGVPD 60
DB 1 DIVMTQSHKFMSTVGVDRVSIICKASQDVGAVDMYQKQSQPKLLIYMASTRHRTGVPD 60
Oy 61 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTRLEK 107
DB 61 RFTGSGSGDTFTLTINVOSEDLADYFCQYNSYPLTFGAGTRLEK 107

RESULT 9
US-08-484-537-50
Sequence 50, Application US/08/484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:

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2 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
2 CURRENT APPLICATION DATA:
2 SOFTWARE: Patent In Release #1.0, Version #1.25
2 CLASSIFICATION: 435
2 PRIOR APPLICATION NUMBER: US/08/484,537
2 FILING DATE:
2 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
2 SOFTWARE: Patent In Release #1.0, Version #1.30
2 CLASSIFICATION: 435
2 PRIOR APPLICATION NUMBER: PCT/JP93/00039
2 FILING DATE: 14-JAN-1993
2 ATTORNEY/AGENT INFORMATION:
2 NAME: Bromdy, Roger L.
2 REGISTRATION NUMBER: 25,618
2 ADDRESS: 1117 North Market Street, Suite 300
2 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (202) 628-5197
2 TELEFAX: (202) 737-3528
2 INFORMATION FOR SEQ ID NO: 4:
2 SEQUENCE CHARACTERISTICS:
2 LENGTH: 107 amino acids
2 TYPE: amino acid
2 TOPOLOGY: linear
2 MOLECULE TYPE: Protein
2 US-08-491-845-4
2
2 Query Match
2 Best Local Similarity 88.6%; Score 504; DB 1; Length 107;
2 Matches 97; Conservative: 4; Mismatches 8; Indels 0; Gaps 0:
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2 QY 1 DIVMTQSHKFMSTSGVDRVSIITCKASODVGTAVDMYQOKPGSPKLLIYNASTHRTGVPD 60
2 DB 1 DIVMTQSHKFMSTSGVDRVSIITCKASODVGTAVDMYQOKPGSPKLLIYNASTHRTGVPD 60
2
2 QY 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLK 107
2 DB 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLK 107
2
2 RESULT 11
2 US-08-797-689-18
2 Sequence 18, Application US/08/797689
2 Patent No. 5876969
2 GENERAL INFORMATION:
2 APPLICANT: Fleer, Reinhard
2 APPLICANT: Fleer, Reinhard
2 APPLICANT: Guittou, Jean-Dominique
2 APPLICANT: Jung, Gerard
2 APPLICANT: Yeh, Patricia
2 TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
2 TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
2 TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
2 NUMBER OF SEQUENCES: 16
2 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Rhone-Poulenc Rorer Inc.
2 STREET: 500 Arcola Road, 3C43
2 CITY: Collegeville
2 STATE: PA
2 COUNTRY: USA
2 ZIP: 19426
2 COMPUTER READABLE FORM:
2 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: System 7.1
2 SOFTWARE: Word 5.1 (Patent In)
2 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/797,689
2 FILING DATE: 31-JAN-1997
2 CLASSIFICATION: 435
2 PRIOR APPLICATION DATA:
2 PRIOR APPLICATION NUMBER:
2 APPLICATION NUMBER: US 08/256,927
2 FILING DATE: 28-JUL-1994
2 APPLICATION NUMBER: FR 92/01064
2 FILING DATE: 31-JAN-1992
2 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: PCT/FR93/00085
2
2
2 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
2 CURRENT APPLICATION DATA:
2 SOFTWARE: Patent In Release #1.0, Version #1.25
2 CLASSIFICATION: 435
2 PRIOR APPLICATION NUMBER: US/08/484,537
2 FILING DATE:
2 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
2 SOFTWARE: Patent In Release #1.0, Version #1.30
2 CLASSIFICATION: 435
2 PRIOR APPLICATION NUMBER: PCT/JP93/00039
2 FILING DATE: 14-JAN-1993
2 ATTORNEY/AGENT INFORMATION:
2 NAME: Bromdy, Roger L.
2 REGISTRATION NUMBER: 25,618
2 ADDRESS: 1117 North Market Street, Suite 300
2 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (202) 628-5197
2 TELEFAX: (202) 737-3528
2 INFORMATION FOR SEQ ID NO: 50:
2 SEQUENCE CHARACTERISTICS:
2 LENGTH: 107 amino acids
2 TYPE: amino acid
2 STRANDEDNESS: single
2 TOPOLOGY: linear
2 MOLECULE TYPE: peptide
2 US-08-484-537-50
2
2 Query Match
2 Best Local Similarity 90.2%; Score 513; DB 4; Length 107;
2 Matches 97; Conservative: 5; Mismatches 5; Indels 0; Gaps 0:
2
2 QY 1 DIVMTQSHKFMSTSGVDRVSIITCKASODVGTAVDMYQOKPGSPKLLIYNASTHRTGVPD 60
2 DB 1 DIVMTQSHKFMSTSGVDRVSIITCKASODVGTAVDMYQOKPGSPKLLIYNASTHRTGVPD 60
2
2 QY 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLK 107
2 DB 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLK 107
2
2 RESULT 10
2 US-08-491-845-4
2 Sequence 4, Application US/08491845
2 Patent No. 5773247
2 GENERAL INFORMATION:
2 APPLICANT: MAEDA, Hiroaki
2 APPLICANT: KIMACHI, Kazuhiko
2 APPLICANT: EDA, Yasuyuki
2 APPLICANT: SHIOSAKI, Kouichi
2 APPLICANT: KISHIMOTO, Akihiro
2 APPLICANT: TOKYOSHI, Sachio
2 TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
2 TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
2 NUMBER OF SEQUENCES: 17
2 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Bromdy and Neimark
2 STREET: 4119 Seventh Street N.W. Ste. 300
2 CITY: Washington
2 STATE: D.C.
2 COUNTRY: USA
2 ZIP: 20004
2 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS

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1 REFERENCE/DOCKET NUMBER: 8648.49USFI
2 TELECOMMUNICATION INFORMATION:
3 TELEPHONE: 612/331-5278
4 TELEFAX: 612/332-9081
5 TELEX:
6
7 INFORMATION FOR SEQ ID NO: 32:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 107 amino acids
10 STRANDS: 1
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 MOLECULE TYPE: protein
14 HYPOTHEetical: NO
15 ANTI-SENSE: NO
16 FRAGMENT TYPE: internal
17 ORIGINAL SOURCE:
18 US-08/767-128-32
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SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-27

Query Match 82.8%; Score 471; DB 4; Length 127;
Best Local Similarity 84.1%; Pred. No. 1.4e-40;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIVMTQSKFMSTSVGDRVSIICKASQDVGVAVDWYQKQPSKLLIYWASTRTFTGVPD 60

DB 21 DIVMTQSKFMSTSVGDRVSIICKASQDVGVAVDWYQKQPSKLLIYWASTRTFTGVPD 80

QY 61 RFTGSGSGDTFTLTINWQSEDLADYFCQQNSYPLTFGAGTMLDK 107

DB 81 RFTGSGSGDTFTLTINWQSEDLADYFCQQNSYPLTFGAGTMLDK 127

RESULT 14

US-08-653-402B-4
Sequence 4; Application US/08653402B
Patent No. 5969107
GENERAL INFORMATION:
APPLICANT: CARCELLER, Ana
INVENTOR: CARCELLER, Ana; Leisbet
APPLICANT: GOREN, Alicia
INVENTOR: GOREN, Alicia
APPLICANT: ADEN, Jaume
INVENTOR: ADEN, Jaume
TITLE OF INVENTION: Anti-Idiotypic antibodies which induce an
immune response against epidermal growth factor receptor.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653.402B
FILING DATE: 24-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95107967.2
FILING DATE: 26-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
TELEPHONE: 703-243-6410
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-402B-4

Query Match 82.8%; Score 468; DB 2; Length 147;
Best Local Similarity 84.1%; Pred. No. 3.4e-40;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVMTQSKFMSTSVGDRVSIICKASQDVGVAVDWYQKQPSKLLIYWASTRTFTGVPD 60

DB 25 DIVMTQSKFMSTSVGDRVSIICKASQDVGVAVDWYQKQPSKLLIYLASNRTFTGVPD 84

QY 61 RFTGSGSGDTFTLTINWQSEDLADYFCQQNSYPLTFGAGTMLDK 107

DB 85 RFTGSGSGDTFTLTINWQSEDLADYFCQQNSYPLTFGAGTMLDK 131

RESULT 15

US-08-398-613A-20
Sequence 20; Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Sherman
INVENTOR: Robert, Carol Anne
APPLICANT: Kim, Kyung Jin
INVENTOR: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammato
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
STREET: 460 California Street, Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398.613A
FILING DATE: 01-MAR-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/705864
APPLICATION NUMBER: 08/705864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-8899
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-398-613A-20

Query Match 82.1%; Score 467; DB 1; Length 123;
Best Local Similarity 83.2%; Pred. No. 3.5e-40;
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVMTQSKFMSTSVGDRVSIICKASQDVGVAVDWYQKQPSKLLIYWASTRTFTGVPD 60

DB 1 DIVMTQSKFMSTSVGDRVSIICKASQDVGVAVDWYQKQPSKLLIYWASTRTFTGVPD 60

QY 61 RFTGSGSGDTFTLTINWQSEDLADYFCQQNSYPLTFGAGTMLDK 107

DB 61 RFTGSGSGDTFTLTINWQSEDLADYFCQQNSYPLTFGAGTMLDK 107

Search completed: July 21, 2003, 13:32:26
Job time : 12.5676 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2003, 13:32:31 ; Search time 32.2928 Seconds
(without alignments)
393,503 Million cell updates/sec

Title: US-09-929-546-19

Perfect score: 569

Sequence: 1 DIVMTQSHKFMSTSVGDRVS.....CQQINSYPLTFGAGTMLDLK 107

Scoring table:

BLOSUM62

Gapop 10.0, Dextp 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications:AA:*

- 1: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 2: /cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2.6/ptodata/1/pubpaa/US06_PUBOMB.pep.*
- 5: /cgn2.6/ptodata/1/pubpaa/US07_PUBOMB.pep.*
- 6: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 7: /cgn2.6/ptodata/1/pubpaa/US08_PUBOMB.pep.*
- 8: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 9: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pep1.*
- 10: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pep2.*
- 11: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pep3.*
- 12: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 13: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep1.*
- 14: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep2.*
- 15: /cgn2.6/ptodata/1/pubpaa/US10_PUBOMB.pep.*
- 16: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 17: /cgn2.6/ptodata/1/pubpaa/US60_PUBOMB.pep.*

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	100.0	107	12	US-09-929-546-19
2	569	100.0	107	12	US-09-929-546-19
3	476	83.7	107	12	US-09-874-141-9
4	476	83.7	133	12	US-09-874-141-51
5	472	83.0	249	11	US-09-984-186-18
6	472	83.0	249	15	US-10-237-667-18
7	472	83.0	249	15	US-10-237-708-18
8	472	83.0	249	15	US-10-237-866-18
9	472	83.0	249	15	US-10-237-871-18
10	472	83.0	249	15	US-10-237-871-18
11	471	82.8	127	12	US-09-749-871-27
12	471	82.8	333	15	US-10-059-261-61
13	469	82.4	331	15	US-10-059-261-169
14	467	82.1	123	12	US-09-726-258-17
15	465	81.7	240	15	US-10-096-246-36
16	465	81.7	245	11	US-09-956-086-5

17	465	81.7	245	11	US-09-956-087-5
18	465	81.7	265	11	US-09-983-580-5
19	465	81.7	265	11	US-09-983-580-5
20	465	81.7	265	11	US-09-983-580-5
21	465	81.7	265	11	US-09-983-580-5
22	463	81.4	240	15	US-10-096-246-37
23	463	81.4	240	15	US-10-096-246-35
24	461	81.0	480	15	US-10-136-793A-59
25	460	80.8	107	15	US-10-184-300A-5
26	460	80.8	128	8	US-08-779-784-36
27	457	80.3	107	15	US-10-184-300A-6
28	457	80.3	107	15	US-10-184-300A-6
29	455	80.0	239	10	US-09-887-853-33
30	455	80.0	250	11	US-09-887-853-2
31	454	79.8	107	15	US-10-184-300A-4
32	454	79.8	108	11	US-09-949-559-104
33	454	79.8	108	12	US-09-875-221A-104
34	450	79.1	239	15	US-10-096-246-32
35	449	79.1	239	15	US-10-096-246-32
36	449	79.1	239	15	US-10-096-246-32
37	449	78.9	131	12	US-09-509-098-130
38	449	78.9	131	12	US-09-269-921-104
39	449	78.9	131	14	US-09-509-098-2
40	448	78.7	107	12	US-10-218-253-104
41	444.5	78.1	124	10	US-09-874-141-3
42	444.5	78.1	124	10	US-09-802-077-4
43	444.5	78.1	124	10	US-09-802-096-4
44	444.5	78.1	124	10	US-09-802-096-4
45	441	77.5	107	12	US-10-096-246-13
					US-09-509-098-134

ALIGNMENTS

RESULT 1
US-09-929-665-19
Sequence 19, Application US/0929665
Publication No. US20030003101A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: Lois M. Kwasiroch: B2L 242/024
PRIORITY CLAIMING DATE: 2001-08-13
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/357,704
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-09-929-665-19

Query Match	100.0%	Score	569	DB 12	Length	107	
Best Local Similarity	100.0%	Pred. No.	3.1e-49				
Matches	107	Conservative	0	Mismatches	0	Gaps	0
QY	1	DIWMTQSHKFMSTSVGDRVSITCKASDVGVDVWQKQPSKLLIYWASTRTFTGVPD	60				
Db	1	DIWMTQSHKFMSTSVGDRVSITCKASDVGVDVWQKQPSKLLIYWASTRTFTGVPD	60				
QY	61	RFTGSGSGDTFTLTINWQSEADYFCQYNSYPLTFGAGTMLDK	107				
Db	61	RFTGSGSGDTFTLTINWQSEADYFCQYNSYPLTFGAGTMLDK	107				

4

FILING DATE: 29-Oct-2001
CLASSIFICATION DATA: <Unknown>
PRIORITY APPLICATION NUMBER:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JAN-1993
APPLICATION NUMBER: PCT/FR93/00085
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: STS2006-US
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-984-186-18

Query Match 83.08; Score 472; DB 11; Length 249;
Best Local Similarity 83.24; Pred. No. 3.le-39;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 DIVMTQSHKFMSTVSGVRISLIICKASODVTAVMYTQOKPQSQPKLLIYWASTRHGTGVPD 60
DB 143 NIQLTPSPMSNSTVSGVRISLTCKASQDVTSVMYQOKPQSQPKLLIYWASTRHGTGVPD 202

OY 61 RFTGSGSDTDITLTVNSQVEDSLADYFCQYNYSPLTFGCAGTMLDLK 107
DB 203 RFTGSGSDTDITLTVNSQVEDSADYFCQYSSYPMTFGGTTKLEIK 249

RESULT 6
US-10-237-667-18
Sequence 18, Application US/10237667
Publication No. US2003022308A1
GENERAL INFORMATION:
APPLICANT: Floor, Reinhard
Fournier, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,667
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-Jan-1997

FILING DATE: 29-Oct-2001
CLASSIFICATION DATA: <Unknown>
PRIORITY APPLICATION NUMBER:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JAN-1993
APPLICATION NUMBER: PCT/FR93/00085
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: STS2006-US
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-237-667-18

Query Match 83.08; Score 472; DB 11; Length 249;
Best Local Similarity 83.24; Pred. No. 3.le-39;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 DIVMTQSHKFMSTVSGVRISLIICKASODVTAVMYTQOKPQSQPKLLIYWASTRHGTGVPD 60
DB 143 NIQLTPSPMSNSTVSGVRISLTCKASQDVTSVMYQOKPQSQPKLLIYWASTRHGTGVPD 202

OY 61 RFTGSGSDTDITLTVNSQVEDSLADYFCQYNYSPLTFGCAGTMLDLK 107
DB 203 RFTGSGSDTDITLTVNSQVEDSADYFCQYSSYPMTFGGTTKLEIK 249

RESULT 7
US-10-237-708-18
Sequence 18, Application US/10237708
Publication No. US20030036170A1
GENERAL INFORMATION:
APPLICANT: Floor, Reinhard
Fournier, Alain
Gultion, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 31-Jan-1992

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: TELECOMMUNICATION INFORMATION
:   TELEPHONE: (610) 454-3839
:   TELEFAX: (610) 454-3808
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 249 amino acids
:   TYPE: amino acid
:   ORGANISM: Homo sapiens
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 18:
: US-10-237-866-18
:
: Query Match      83.0% Score 472; DB 15; Length 249;
: Best Local Similarity 83.2%; Pred. No. 3.1e-39;
: Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
:
: OY    1 DTVMTGSHKPMSTVSGVDRTSVITCKASQDVTAVDWFOOKQGSPKKLIYIAWSTRHTGVDP 60
:       I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: DB    143 NTLQTSPMSMSTVSGVDRTSVITCKASQDVTAVDWFOOKQGSPKKLIYIAWSTRHTGT 202
:
: OY    61 RFTGSSGDPTLTITNVQSEDLADYFCQYRYSRYPLTGAGTMDLLA 107
:       I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: DB    203 RFTGSSGDPTLTISNWSQESNDTPCOQYSTPMTFGTGLLEIK 249
:
: RESULT 9
: US-10-237-871-18
: Publication No. Application US/10237871
: Sequence 18; US20030036172AI
: GENERAL INFORMATION:
:   Filer: Reinhard
:   Examiner: Robert
:   Attorney: Jean-Dominique
:   Jung, Gerard
:   Yeh, Patrice
: TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
:
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rhone-Poulenc Rorer Inc.
: STREET: 500 Arcola Road, 3C43
: CITY: Collegeville
: STATE: PA
: COUNTRY: USA
: ZIP: 19426
: COMPUTER-READABLE FORM:
: INPUT FILE: PEPHY disk
: COMPUTER: Macintosh
: OPERATING SYSTEM: System 7.1
: SOFTWARE: Word 5.1 (PatentIn)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/237, 871
: FILING DATE: 10-Sep-2002
: CLASSIFICATION: <unknown>
: PRIOR ART CITATIONS:
: APPLICATION NUMBER: US/08/757, 689
: FILING DATE: 31-JAN-1997
: APPLICATION NUMBER: US 08/256, 927
: FILING DATE: 28-JUL-1994
: APPLICATION NUMBER: FR 92/01064
: FILING DATE: 31-JAN-1992
: APPLICATION NUMBER: EP 92/00199
: FILING DATE: 20-FEB-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith Ph.D., Julie K.
: REGISTRATION NUMBER: P-38,619
: REFERENCE/DOCKET NUMBER: ST92006-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610) 454-3839
: TELEFAX: (610) 454-3808
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:

```

[illegible]

Db 81 RTGSGSGDTLTTTWSQEDLADYFCQOYNSTPRFGGTKLQK 127
 |||||

RESULT 12

US-10-059-261-61
 ; Sequence 61, Application US/10059261
 ; GENERAL INFORMATION: US20030077826A1
 ; APPLICANT: EDELMAN, LENA
 ; APPLICANT: BRIAND, JEAN-PAUL
 ; APPLICANT: ETIENNE DANIEL FRANCOIS
 ; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
 ; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC
 ; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
 ; TITLE OF INVENTION: (PTPC)
 ; FILE REFERENCE: 03495.0216
 ; CURRENT APPLICATION NUMBER: US/10/059,261
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR FILING DATE: 2001-02-02
 ; NUMBER OF SEQ ID NOS: 325
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 61
 ; LENGTH: 333
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-ScFv461
 ; OTHER INFORMATION: peptide sequence
 US-10-059-261-61

Query Match 82.8%; Score 471; DB 15; Length 333;
 Best Local Similarity 84.1%; Pred. No. 5.4e-39;
 Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 Oy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAQVMTQKQSQPKLLIYMASTRHTGVPD 60
 Db 221 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAQVMTQKQSQPKLLIYMASTRHTGVPD 280
 Oy 61 RTGSGSGDTLTTTWSQEDLADYFCQOYNSTPRFGGTKLQK 107
 Db 281 RTGSGSGDTLTTTWSQEDLADYFCQOYNSTPRFGGTKLQK 327

RESULT 13

US-10-059-261-169
 ; Sequence 169, Application US/10059261
 ; GENERAL INFORMATION: US20030077826A1
 ; APPLICANT: EDELMAN, LENA
 ; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
 ; APPLICANT: BRIAND, JEAN-PAUL
 ; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
 ; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC
 ; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
 ; TITLE OF INVENTION: (PTPC)
 ; FILE REFERENCE: 03495.0216
 ; CURRENT APPLICATION NUMBER: US/10/059,261
 ; CURRENT FILING DATE: 2002-08-29
 ; PRIOR FILING DATE: 2001-02-02
 ; NUMBER OF SEQ ID NOS: 325
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 169
 ; LENGTH: 331
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-ScFv350
 ; OTHER INFORMATION: peptide sequence
 US-10-059-261-169

Query Match 82.4%; Score 469; DB 15; Length 331;
 Best Local Similarity 83.2%; Pred. No. 8.4e-39;
 Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 Oy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAQVMTQKQSQPKLLIYMASTRHTGVPD 60
 Db 219 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAQVMTQKQSQPKLLIYMASTRHTGVPD 278
 Oy 61 RTGSGSGDTLTTTWSQEDLADYFCQOYNSTPRFGGTKLQK 107
 Db 279 RTGSGSGDTLTTTWSQEDLADYFCQOYNSTPRFGGTKLQK 325

RESULT 14

US-09-726-258-17
 ; Sequence 17, Application US/09726258
 ; GENERAL INFORMATION: US20030021790A1
 ; APPLICANT: Genentech, Inc., Hsael, Vanessa
 ; APPLICANT: Genentech, Inc., Hsael, Vanessa
 ; APPLICANT: Leonard, Steven R.
 ; APPLICANT: Presta, Leonard R.
 ; APPLICANT: Shahrokhi, Zahra
 ; APPLICANT: Zapata, Gerardo A.
 ; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
 ; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
 ; CURRENT APPLICATION NUMBER: 09/09726258
 ; CURRENT FILING DATE: 2002-08-29
 ; ADDRESS: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMMERCIAL AVAILABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: 09/09726,258
 ; FILING DATE: 2002-08-29
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; FILING DATE: 09/234,182
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/094003
 ; FILING DATE: 24-JUL-1998
 ; INVENTOR/ASSIGNOR:
 ; NAME: Long, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: P10859A-1A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5530
 ; TELEFAX: 650/952-9881
 ; INFORMATION CHARACTERISTICS:
 ; SEQUENCE CHARACTERISTICS: 17;
 ; LENGTH: 123 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 US-09-726-258-17

Query Match 82.1%; Score 467; DB 12; Length 123;
 Best Local Similarity 83.2%; Pred. No. 8.4e-39;
 Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAQVMTQKQSQPKLLIYMASTRHTGVPD 60
 Db 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAQVMTQKQSQPKLLIYMASTRHTGVPD 60
 Oy 61 RTGSGSGDTLTTTWSQEDLADYFCQOYNSTPRFGGTKLQK 107
 Db 1 RTGSGSGDTLTTTWSQEDLADYFCQOYNSTPRFGGTKLQK 107

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DB      61  RFTGSGSGTDFLTITSHVQSEDLADYFCQQYNIELYFTFGPGTKLEK 107

RESULT 15
US-10-096-246-36
: Sequence 36, Application US/10096246
: Publication No. US20030100060A1
: GENERAL INFORMATION:
: APPLICANT: The Minister of National Defence, Government of Canada
: APPLICANT: Fulton, R E
: APPLICANT: Rasmussen, E
: APPLICANT: Nagata Leslie
: TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M
: FILE REFERENCE: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
: CURRENT APPLICATION NUMBER: US/10/096,246
: CURRENT FILING DATE: 2002-03-13
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: SeqScribe
: SEQ ID NO 36
: LENGTH: 240
: TYPE: PR1
: ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-36

Query Match      81.7%  Score 4651  DB 15:  Length 240:
Seq. Loc. Similarity 78.5%  Pos 15-35
Matches 84:  Conservative 12:  Mismatches 11:  Indels 0:  Gaps 0:

Qy      1  DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYNASTHTGTGVPD 60
DB      133  DIELTQSPNLSLSTSGDRIRITCKASQDVTAVGWYQKPGQSPKLLIPMSSTHTGTGVPD 192
Qy      61  RFTGSGSGTDFLTITSHVQSEDLADYFCQQYNIELYFTFGAGTMDLK 107
DB      193  RFTGSGSGTDFLTITSHVQSEDLADYFCQYSSYPTFGSGTKLEIK 239

Search completed: July 21, 2003, 13:46:34
Job time : 33.2928 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2003, 13:23:15 ; Search time 23.6171 Seconds
(without alignments)
435.548 Million cell updates/sec

Title: US-09-929-546-19

Perfect score: 569

Sequence: 1 DIVMTQSHKFMSTVSGDRVS.....COQYNSVPLTSGAGTMDLX 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	526	92.4	117	2 S42466	Ig kappa chain v r
2	499	87.7	131	2 PL0207	anti-idiotypic ant
3	483	84.9	152	2 S30751	Ig kappa chain pre
4	462	81.2	107	2 A28195	Ig kappa chain v r
5	452	81.2	108	2 PL0404	anti-DNA autoantib
6	452	79.4	107	2 S32192	Ig kappa chain v r
7	452	79.4	107	2 S32191	Ig kappa chain v r
8	450	79.1	107	2 S32191	Ig kappa chain v r
9	446	78.4	149	1 KVS11	Ig kappa chain pre
10	444.5	78.1	108	2 B4371	Ig kappa chain v r
11	440	77.3	119	2 P00265	Ig kappa chain v r
12	436	76.5	128	2 A71159	Ig light chain v r
13	432	75.9	106	2 H38602	Ig kappa chain v r
14	432	75.9	106	2 H38602	Ig kappa chain v r
15	423	74.3	107	2 S09967	Ig kappa chain v r
16	416.5	73.2	108	2 PL0083	Ig kappa chain v r
17	416	73.1	90	2 S38561	Ig light chain v r
18	416	73.1	94	2 F33730	Ig kappa chain v r
19	408	71.7	93	2 S38559	Ig light chain v r
20	405	71.2	127	2 S04577	Ig light chain v r
21	402	70.3	107	2 S38602	Ig kappa chain v r
22	400	70.3	107	2 S38602	Ig kappa chain v r
23	394	69.2	90	2 I38601	Ig kappa chain pre
24	394	69.2	136	1 KVS21	Ig kappa chain v r
25	393.5	69.2	106	2 PL0088	Ig kappa chain v r
26	393	69.1	111	2 D37266	Ig kappa chain v r
27	393	69.1	145	2 PL0014	Ig kappa chain pre
28	387.5	68.1	225	2 S37484	Ig kappa chain - m
29	384	67.5	113	2 A49260	antitumor monoclon

30 383 67.3 113 2 PL0263 Ig kappa chain v r
31 381 67.0 107 2 S36264 Ig lambda chain v
32 381 67.0 134 2 PC1214 Ig kappa chain pre
33 379.5 66.7 139 2 S25049 Ig kappa chain v r
34 379 66.6 107 2 S36268 Ig lambda chain v
35 379 66.6 107 2 S36268 Ig kappa chain v r
36 378 66.4 107 2 S31132 Ig kappa chain v r
37 377 66.3 108 2 S19674 Ig kappa chain v r
38 376.5 66.2 118 2 P70356 Ig kappa chain - h
39 376 65.1 132 2 S40334 Ig kappa chain v r
40 375 65.9 108 1 K40DUX Ig kappa chain v r
41 374 65.7 134 2 S68232 Ig light chain v r
42 374 65.7 112 2 S09970 Ig kappa chain v r
43 373.5 65.6 112 2 S09970 Ig kappa chain v r
44 372 65.4 88 2 A37262 Ig kappa chain v r
45 372 65.4 112 2 F30538 Ig kappa chain v r

ALIGNMENTS

RESULT 1

S42466

Ig kappa chain v region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S42466 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Submitted: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Submitted: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

A:Reference number: S42466

A:Accession: S42466

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 <SI>

A:Cross-references: EMBL:X73106; NID:g460824; PIDN:CHAS4398.1; PTD:g460825

A:Keywords: heterotrimer; immunoglobulin homology

F:26-100/Domain: immunoglobulin homology <IM>

Query Match 92.4%; Score 526; DB 2; Length 117;

Best Local Similarity 91.6%; Pred. No. 5.7e-42;

Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DIVMTQSHKFMSTVSGDRVSITCKASQDVGTAATQKQKQSQKLLITWASTHTHTGVPD 60

Db 11 DIVMTQSHKFMSTVSGDRVSITCKASQDVGTAATQKQKQSQKLLITWASTHTHTGVPD 70

Oy 61 RFTGSGSDGDTLTITNVSQEDLADYFCQYNSVPLTSGAGTMDLX 107

Db 71 RFTGSGSDGDTLTITNVSQEDLADYFCQYNSVPLTSGAGTMDLX 117

RESULT 2

PL0207

anti-idiotypic antibody E225, kappa chain v region precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: PL0207 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Submitted: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Submitted: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

A:Reference number: 27, 429-433, 1990

A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reac

A:Accession: PL0207

A:Molecule type: mRNA

A:Residues: 1-131 <SO>

A:Cross-references: EMBL:X73106; NID:g460824; PIDN:CHAS4398.1; PTD:g460825

A:Keywords: heterotrimer; immunoglobulin homology

F:1-20/Domain: immunoglobulin homology <SI>

F:36-110/Domain: immunoglobulin homology <IM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-117/Region: complementarity-determining 3

F:116-127/Region: J region

C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S32192
 A:Reference number: S32185
 A:Reference number: S32185
 A:Accession: S32192
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-107 <I2U>
 A:Cross-references: EMBL:X70097; MID:g288262; PID:CAA49700.1; PID:g288263
 A:Notes: This sequence is inconsistent with the nucleotide translation
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-30/Domain: immunoglobulin homology <IM>

Query Match 79.1%; Score 452; DB 2; Length 107;
 Best Local Similarity 81.3%; Pred. No. 3.8e-35;
 Matches 87; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 60
 DB 1 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 60
 QY 61 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 107
 DB 61 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 107

RESULT 8
 S32191
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S32191
 A:Reference number: S32185
 A:Accession: S32191
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-107 <I2U>
 A:Cross-references: EMBL:X70095; MID:g288260; PID:CAA49700.1; PID:g288261
 A:Notes: This sequence is inconsistent with the nucleotide translation
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-30/Domain: immunoglobulin homology <IM>

Query Match 79.1%; Score 450; DB 2; Length 107;
 Best Local Similarity 81.3%; Pred. No. 5.8e-35;
 Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
 QY 1 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 60
 DB 1 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 60
 QY 61 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 107
 DB 61 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 107

RESULT 9
 KWS11
 Ig kappa chain precursor V region (MPC11) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 21-Jan-2000
 C:Accession: A90823; A90753; A90298; A01916
 A:Reference number: S32185
 A:Accession: A90823; A90753; A90298; A01916
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-71 <KEL>
 A:Note: The sequence was determined from the differentiated gene
 R:Rabbits, T.H.; Hamlyn, P.H.; Matthysens, G.; Roe, B.A.

Can. J. Biochem. 58, 176-187, 1980
 A:Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
 A:Reference number: S32185
 A:Reference number: A90753; MID:60176534; PMID:6245773
 A:Molecule type: mRNA
 A:Residues: 41-149 <RAB>
 R:Smith, G.P.
 Biochem. J. 171, 337-347, 1978
 A:Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC
 A:Reference number: A90298; MID:78186617; PMID:418775
 A:Contents: myeloma protein MPC11
 A:Accession: A90298
 A:Molecule type: protein
 A:Residues: 30-145 <SMI>
 A:Note: The amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not
 C:Comment: The mature chain has 12 additional residues at its amino end, due to a tan
 42 corresponds to the amino-terminal residue of typical kappa chains.
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (L)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: duplication; heterotrimer; immunoglobulin
 F:1-29/Domain: signal sequence; #status predicted <SIG>
 F:30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
 F:57-131/Domain: immunoglobulin homology <IM>
 F:64-129/Disulfide bonds: #status predicted

Query Match 78.4%; Score 446; DB 1; Length 149;
 Best Local Similarity 80.4%; Pred. No. 1.9e-34;
 Matches 86; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 1 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 60
 DB 42 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 101
 QY 61 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 107
 DB 102 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 148

RESULT 10
 B44371
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Apr-1993 #sequence_revision 30-Apr-1993 #text_change 21-Jan-2000
 C:Accession: B44371
 R:Avala, M.; Duenas, A.; Vazquez, J.; Menendez, A.; Silva, A.; Gavilondo,
 BioTechniques 13, 790-799, 1992
 A:Title: Bacterial single-chain antibody fragments, specific for carcinoembryonic ant
 A:Reference number: A44371; MID:95042004; PMID:1418961
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <RA>
 A:Cross-references: GB:S49457; MID:g259513; PID:AA824087.1; PID:g259514
 A:Note: This sequence is inconsistent with the nucleotide translation
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-30/Domain: immunoglobulin homology <IM>

Query Match 78.1%; Score 444.5; DB 2; Length 108;
 Best Local Similarity 80.6%; Pred. No. 1.9e-34;
 Matches 87; Conservative 8; Mismatches 12; Indels 1; Gaps 1;
 QY 1 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 60
 DB 1 DVTMTQSHKFMSTSGVDRVSTICRKSQDVTAVDYQKQSPKLLIYASTRTGVPD 60
 QY 61 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 107
 DB 61 RFTGSGSGDFTLTITNVQSEDLADYFCQVNSYPLTFGAGTMDLK 108

RESULT 11

P00265
Ig kappa chain V region (MC1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: P00265
R:Lozman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A:Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal
A:Reference number: P00265; NUID:92039046; PMID:1937027
A:Accession: P00265
A:Residues: 1-119 <G>S
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-119 <G>S
A:Cross-references: GB:M59985
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:28-102/Domain: Immunoglobulin homology <IMM>
F:28-102/Region: Complementarity-determining 1
F:62-69/Region: Complementarity-determining 2
F:101-109/Region: Complementarity-determining 3
Query Match 77.3%; Score 440; DB 2; Length 119;
Best Local Similarity 79.4%; Pred. No. 5.5e-34;
Matches 85; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
Qy 1 DIVMTQSHKFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPD 60
Db 13 DIVMTQSHKFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPD 72
Qy 61 RFTGSGSGDTFTLTINNVQSEDADYFCQYNSYPLTFGAGTMDLK 107
Db 73 RFTGSGSGDTFTLTINNVQSEDADYFCQYNSYPLTFGAGTMDLK 119
RESULT 12
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Accession: A47159
Ig lambda chain V region (CEA-specific mAb T84.66) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A47159
R:Galda, C.; J. Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumeister, M.
Gene 105, 283-284, 1991
A:Title: Molecular characterization of a cloned idiotype cascade containing a network
A:Reference number: A47159; NUID:93300804; PMID:7686150
A:Accession: A47159
A:Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-128 <G>S
A:Experimental source: hybridoma 656.C4
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: Immunoglobulin homology <IMM>
Query Match 76.6%; Score 436; DB 2; Length 128;
Best Local Similarity 77.6%; Pred. No. 1.4e-33;
Matches 83; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
Qy 1 DIVMTQSHKFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPD 60
Db 21 DIVMTQSHKFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPD 80
Qy 61 RFTGSGSGDTFTLTINNVQSEDADYFCQYNSYPLTFGAGTMDLK 107
Db 81 RFTGSGSGDTFTLTINNVQSEDADYFCQYNSYPLTFGAGTMDLK 127
RESULT 13
Ig light chain V region (clone 83-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1072
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibo

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; NUID:92381444; PMID:1512540
A:Accession: PH0971
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-98 <TIL>
A:Experimental source: B cell, strain (NZB x NZW)F1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: Immunoglobulin homology <IMM>
Query Match 76.3%; Score 434; DB 2; Length 98;
Best Local Similarity 83.7%; Pred. No. 1.6e-33;
Matches 82; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
Qy 1 DIVMTQSHKFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPD 60
Db 1 DIVMTQSHKFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPD 60
Qy 61 RFTGSGSGDTFTLTINNVQSEDADYFCQYNSYPLTF 98
Db 61 RFTGSGSGDTFTLTINNVQSEDADYFCQYNSYPLTF 98
RESULT 14
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Accession: A38601
Ig kappa chain V region (3A3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: A38601
R:Goehorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <GOS>
A:Cross-references: GB:M57985; NUID:g196416; PIDN:AA63366.1; PID:g196417
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-42/Domain: Immunoglobulin homology <IMM>
Query Match 75.9%; Score 432; DB 2; Length 100;
Best Local Similarity 81.8%; Pred. No. 2.5e-33;
Matches 81; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
Qy 9 KFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPDFTGSGSG 68
Db 1 KFMSTVSGDRVSVTCCKASQDVGTAVMTQKQPSKLLIYMASTRHTGVPDFTGSGSG 60
Qy 69 TQFTLTINNVQSEDADYFCQYNSYPLTFGAGTMDLK 107
Db 61 TQFTLTINNVQSEDADYFCQYNSYPLTFGAGTMDLK 99
RESULT 15
S09967
Ig kappa chain V-J region (31-9D) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-1996
C:Accession: S09967
R:Reininger, E.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izul, S.
Gene 105, 283-284, 1991
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibo
A:Reference number: S09955; NUID:90269328; PMID:2347362
A:Accession: S09967
A:Molecule type: mRNA
A:Residues: 1-107 <REI>
A:Cross-references: EMBL:X51855
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

Search completed: July 21, 2003, 13:33:22
Job time : 24.6171 secs

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Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	446	78.4	149	1	KV5A_MOUSE	P01633	mus musculus
	2	394	69.2	136	1	KV5B_MOUSE	P01634	mus musculus
	3	375	65.9	108	1	KV1B_HUMAN	P01605	homo sapien
	4	368	65.7	136	1	KV4C_HUMAN	P06362	homo sapien
	5	367	64.5	114	1	KV4A_HUMAN	P01625	homo sapien
	6	367	64.5	114	1	KV4C_HUMAN	P01625	homo sapien
	7	363	63.8	108	1	KV10_HUMAN	P01609	homo sapien
	8	362	63.6	108	1	KV1P_HUMAN	P01608	homo sapien
	9	360.5	63.4	133	1	KV4B_HUMAN	P06313	homo sapien
	10	358	62.9	108	1	KV1V_HUMAN	P04430	homo sapien
	11	356	62.6	108	1	KV1L_HUMAN	P01604	homo sapien
	12	356	62.6	108	1	KV1S_HUMAN	P01611	homo sapien
	13	355	62.4	108	1	KV1T_HUMAN	P01612	homo sapien
	14	352	61.9	108	1	KV5X_MOUSE	P01642	mus musculus
	15	349.5	61.4	129	1	KV3B_HUMAN	P04207	homo sapien
	16	349	61.3	108	1	KV1K_HUMAN	P01603	homo sapien
	17	348	61.2	108	1	KV1O_HUMAN	P01607	homo sapien
	18	347	61.0	108	1	KV5Z_MOUSE	P01643	mus musculus
	19	347	61.0	108	1	KV5L_MOUSE	P01643	mus musculus
	20	344	60.5	108	1	KV1A_HUMAN	P01593	homo sapien
	21	344	60.5	109	1	KV1G_HUMAN	P01599	homo sapien
	22	343.5	60.4	108	1	KV1D_HUMAN	P01626	homo sapien
	23	343.5	60.4	109	1	KV3D_HUMAN	P01594	homo sapien
	24	343	60.3	108	1	KV3B_HUMAN	P01594	homo sapien
	25	343	60.3	108	1	KV5B_MOUSE	P01647	mus musculus
	26	342.5	60.2	109	1	KV3F_HUMAN	P01624	homo sapien
	27	342	60.1	108	1	KV1F_HUMAN	P01598	homo sapien
	28	342	60.1	108	1	KV5E_MOUSE	P01646	mus musculus
	29	342	60.1	108	1	KV5O_MOUSE	P01610	mus musculus
	30	341.5	59.9	108	1	KV1R_HUMAN	P01610	homo sapien
	31	341.5	59.9	108	1	KV1R_HUMAN	P01610	homo sapien
	32	339	59.6	108	1	KV5P_MOUSE	P01649	mus musculus
	33	339	59.6	129	1	KV1W_HUMAN	P04431	homo sapien

FT
CHN

FT	CHAIN	30	149	IG KA
FT	CHAIN	30	149	IG KA

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	446	78.4	149	1	KV5A_MOUSE	P01633	mus musculus
	2	394	69.2	136	1	KV5B_MOUSE	P01634	mus musculus
	3	375	65.9	108	1	KV1B_HUMAN	P01605	homo sapien
	4	368	65.7	136	1	KV4C_HUMAN	P06362	homo sapien
	5	367	64.5	114	1	KV4A_HUMAN	P01625	homo sapien
	6	367	64.5	114	1	KV4C_HUMAN	P01625	homo sapien
	7	363	63.8	108	1	KV10_HUMAN	P01609	homo sapien
	8	362	63.6	108	1	KV1P_HUMAN	P01608	homo sapien
	9	360.5	63.4	133	1	KV4B_HUMAN	P06313	homo sapien
	10	358	62.9	108	1	KV1V_HUMAN	P04430	homo sapien
	11	356	62.6	108	1	KV1L_HUMAN	P01604	homo sapien
	12	356	62.6	108	1	KV1S_HUMAN	P01611	homo sapien
	13	355	62.4	108	1	KV1T_HUMAN	P01612	homo sapien
	14	352	61.9	108	1	KV5X_MOUSE	P01642	mus musculus
	15	349.5	61.4	129	1	KV3B_HUMAN	P04207	homo sapien
	16	349	61.3	108	1	KV1K_HUMAN	P01603	homo sapien
	17	348	61.2	108	1	KV1O_HUMAN	P01607	homo sapien
	18	347	61.0	108	1	KV5Z_MOUSE	P01643	mus musculus
	19	347	61.0	108	1	KV5L_MOUSE	P01643	mus musculus
	20	344	60.5	108	1	KV1A_HUMAN	P01593	homo sapien
	21	344	60.5	109	1	KV1G_HUMAN	P01599	homo sapien
	22	343.5	60.4	108	1	KV1D_HUMAN	P01626	homo sapien
	23	343.5	60.4	109	1	KV3D_HUMAN	P01594	homo sapien
	24	343	60.3	108	1	KV3B_HUMAN	P01594	homo sapien
	25	343	60.3	108	1	KV5B_MOUSE	P01647	mus musculus
	26	342.5	60.2	109	1	KV3F_HUMAN	P01624	homo sapien
	27	342	60.1	108	1	KV1F_HUMAN	P01598	homo sapien
	28	342	60.1	108	1	KV5E_MOUSE	P01646	mus musculus
	29	342	60.1	108	1	KV5O_MOUSE	P01610	mus musculus
	30	341.5	59.9	108	1	KV1R_HUMAN	P01610	homo sapien
	31	341.5	59.9	108	1	KV1R_HUMAN	P01610	homo sapien
	32	339	59.6	108	1	KV5P_MOUSE	P01649	mus musculus
	33	339	59.6	129	1	KV1W_HUMAN	P04431	homo sapien


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RESULT 4
144A_HUMAN
AC P03162: STANDARD; PRT: 108 AA.
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RX MEDLINE=95086080; PubMed=7993911;
RX Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RX Solomon A., Stevens J., Schiffer M.; two homologous proteins:
RX structural origin of altered domain interactions in immunoglobulin
RX light-chain dimers.;
RX Biochemistry 33:14848-14857(1994).
[2]
RN SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RX Poppe R.A., Solomon A., Panagiotopoulos N., Schiffer M.,
RX "Characterization and preliminary crystallographic data on the VL-
RX related fragment of the human Ki Bence Jones protein Nat.;"
RX J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB: 1MTL; 01-NOV-94.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; 19-V.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT DOMAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 50 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 51 57 FRAMEWORK-2.
FT DOMAIN 58 68 FRAMEWORK-3.
FT DOMAIN 69 77 FRAMEWORK-4.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 107 FRAMEWORK-3.
FT DISULFID 108 109 BY SIMILARITY.
FT NON_TER 108 109 TN -> SD (IN REF. 2).
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0AE597 CRC64;
Query Match 65.9%; Score 375; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 4,8e-34;
Matches 68; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 DVTYQSHKFMSTVSGDRVSIITCASODVGTAVDYVYQKQPSKLLIYWASTRTGVPD 60
DB 1 DVTQTPGSLASGVGRVSIITCASODITVYVNFQRPQAPKRVLLIGASILETGVPD 60
QY 61 RTFTSGSGSDTFTLTINQVSEDADYFCQVNSYPLTFAGTGMDLK 107
DB 61 RFSGSGSGSDTFTFTSISSLEDIATVYCCQVDTLPDTFGSGTKVDIK 107

RESULT 5
144A_HUMAN
AC P03162: STANDARD; PRT: 134 AA.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DE Ig kappa chain V-I region B17 precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RX Schneider M., Hilschmann N.;
RX "The primary structure of a monoclonic immunoglobulin-L-chain of

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P04430:
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region BAN.
DB
DS Homo sapiens (Human).
OS Homo sapiens (Human).
OC Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxId=9606; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RNM SEQUENCE.
MEDLINE=66174817; PubMed=3083240;
Dwight F.E., O'Connor T.P., Benson M.D.;
Polyomorphism in the kappa L primary (AL) amyloid protein (BAN). *;
Mol Cell Biochem. 1987 Jul;81(1-2):78(1986).
PIR: A01878; K1HUBN.
DR HSSP: P03362; IWLK.
OR InterPro: IPRO03006; Ig_MHC.
DR InterPro: IPRO03596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGv; 1.
DR ImmunoGlobulin V region; Amyloid
protein; Immunoglobulin V region; Framework-1
DOMAIN 24 34
FFT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FFT DOMAIN 35 49 FRAMEWORK-2.
FFT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FFT DOMAIN 57 88 FRAMEWORK-3.
FFT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FFT DOMAIN 98 107 FRAMEWORK-4.
FFT DOMAIN 98 107 BY SIMILARITY.
FFT NQKER 108 108
SEQUENCE 108 AA: 11840 MW: CD3FD94F6E6FD37 CMC64;

Query Match 62.9%; Score 358; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 3,4e-32;
Matches 68; Conservative 14; Mismatches 25; Indels 0; Gaps 0

Oy 1 DVMTGSHFHSYGVCHVSTCKASDVGTATDYKVQFGSGPKLLIYNSTRHTCVD 60
DB 1 DQLQTSPSSLASGVGRVTITCRASGYVTVYVAMFQMGKPKAKSLIVDASTLQSQVPS 60
Oy 61 RFTGSGSGDTFLITINVGSELDADYFCOOTNSYLPTAGCMPLDLK 107
DB 61 NFTGSGSGDTFLITISSLPQDFATYYCOQNSYTFPGQGKVIK 107

RESULT 11
KVLL_HUMAN STANDARD; PRS; 108 AA.
AC ID KVLL_HUMAN STANDARD; PRS; 108 AA.
AC P01604;
DB 21-JUL-1986 (Rel. 01, Created)
DB 21-JUL-1986 (Rel. 01, Last sequence update)
DB 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OS Homo sapiens (Human).
OC Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxId=9606; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RNM SEQUENCE.
MEDLINE=79237924; PubMed=112021;
Wright M., Riley H.P., Zeller W.C., Jones
sequence of the variable part of a human L-chain of the kappa type.*;
Hoppe-Seyler's z. physiol. Chem. 360:725-734(1979).
RL -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
OR PIR: A01870; K1KHUK.
DR HSSP: P01607; IREI.
DR InterPro: IPRO03006; Ig_MHC.
DR TrEMBL: P01607; Ig_v.
DR SMART: SM00406; IGv; 1.


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DE Ig kappa chain V-V region HP RI6.7.
OC Eukaryotic Vertebrates; Chordata; Craniata; Vertebrates; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=8/2; PubMed=6801658;
RA SUGEN=8/2;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KWSAR.
DR HSSP: P01606; IGV; 1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW CHAIN 1 23
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 44 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 45 56 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 57 68 FRAMEWORK-2.
FT DOMAIN 69 78 FRAMEWORK-3.
FT DOMAIN 79 88 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-5.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11910 MW; A554642C638FF597 CRC64;
SQ SEQUENCE 108 AA; 11910 MW; A554642C638FF597 CRC64;

Query Match 61.9%; Score 352; DB 1; Length 108;
Best Local Similarity 59.8%; Pred. No. 1.5e-31;
Matches 54; Conservative 20; Mismatches 23; Indels 0; Caps 0;

OY 1 DIYMTQSHKFNSTVGDRVSIICAKASODVGVADYVQKQPSKLLIYWASTRTGVPD 60
DB 1 DIYMTQSHKFNSTVGDRVSIICAKASODVGVADYVQKQPSKLLIYWASTRTGVPD 60
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 107
DB 61 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 107
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

DB 81 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 128
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: July 21, 2003, 13:31:53
Job time : 12.5315 secs

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or send an email to license@isb-sib.ch).
CC EMBL: M12740; AAA58992.1;
CC PIR: A01898; K3HUCI.
CC HSSP: P80362; IWTCL.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR003596; IG_V.
CC Pfam: PF00047; Iq; 1.
CC SMART: SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
KW CHAIN 1 129
FT DOMAIN 1 129 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 54 FRAMEWORK-2.
FT DOMAIN 55 69 FRAMEWORK-3.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-4.
FT DOMAIN 109 129 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 61.4%; Score 349.5; DB 1; Length 129;
Best Local Similarity 61.1%; Pred. No. 3.5e-31;
Matches 66; Conservative 19; Mismatches 22; Indels 1; Caps 1;

OY 1 DIYMTQSHKFNSTVGDRVSIICAKASODVGVADYVQKQPSKLLIYWASTRTGVPD 60
DB 21 EIVMTQSPATLVSFGEATLSRCASQSVSNLAWYQKQPPRLIYGASTRTGIPA 80
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 107
DB 81 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 128
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: July 21, 2003, 13:31:53
Job time : 12.5315 secs

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Ig kappa chain V-V region HP RI6.7.
OC Eukaryotic Vertebrates; Chordata; Craniata; Vertebrates; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=8/2; PubMed=6801658;
RA SUGEN=8/2;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KWSAR.
DR HSSP: P01606; IGV; 1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Antiarsonate antibody.
KW CHAIN 1 23
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 44 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 45 56 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 57 68 FRAMEWORK-2.
FT DOMAIN 69 78 FRAMEWORK-3.
FT DOMAIN 79 88 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-5.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11910 MW; A554642C638FF597 CRC64;
SQ SEQUENCE 108 AA; 11910 MW; A554642C638FF597 CRC64;

Query Match 61.9%; Score 352; DB 1; Length 108;
Best Local Similarity 59.8%; Pred. No. 1.5e-31;
Matches 54; Conservative 20; Mismatches 23; Indels 0; Caps 0;

OY 1 DIYMTQSHKFNSTVGDRVSIICAKASODVGVADYVQKQPSKLLIYWASTRTGVPD 60
DB 1 DIYMTQSHKFNSTVGDRVSIICAKASODVGVADYVQKQPSKLLIYWASTRTGVPD 60
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 107
DB 61 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 107
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

DB 81 RFTSGSGDTFTLTINVOSEDLADYFCQOYNSTPLTFGAGTMDLX 128
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
II:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Qy 61 RFTGSGSDTFLTTTWQSEDLADYFCQYNSYPLTFGAGTMDLX 107
Db 61 RFTGSGSDTFLTTTWQSEDLADYFCQYNSYPLTFGAGTMDLX 107

RESULT 2
Q9ULJ74
ID Q9ULJ74 PRELIMINARY: PRT: 99 AA.
AC Q9ULJ74: 2000 (TREMBlrel. 15, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC [11_TaxID=10930;
RN [11_TaxID=10930;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Makiel S., Liao L., Cunningham M.W., Diamond B.:
RA "T-cell-dependent antibody response to the dominant epitope of
RA trepanoidal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RA with lectin immunoglobulin light chain variable region
RA (Fragment).
DR EMBL: AF205032; AAF69330.1; -.
DR HSP: P80362; IWL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 99
FT NON_TER 99
SEQUENCE 99 AA: 10939 MW; 38250E784533324 CRC64;

Query Match 65.0%; Score 370; DB 11; Length 99;
Best Local Similarity 71.7%; Pred. No. 2.6e-33;
Matches 71; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 9 KPMSTVGVDRVSTICKASQDVTADVQYQKQSPKLLIYASTRTHTGVPDFTGSGSG 68
Db 1 KFLVLSAGDRVITTCASQSVNDVAYQYQKQSPKLLIYASNRITGVPDRFTGSGVG 60

Qy 69 TDFLTITNWQSEDLADYFCQYNSYPLTFGAGTMDLX 107
Db 61 TDFLTITNWQSEDLADYFCQYNSYPLTFGAGTMDLX 107

RESULT 3
Q9ULJ79
ID Q9ULJ79 PRELIMINARY: PRT: 108 AA.
AC Q9ULJ79: 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC [11_TaxID=9606;
RN [11_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA Myosin-reactive autoantibodies in rheumatic carditis and normal
RA (Fragment).
DR EMBL: AF035044; RAD56280.1; -.
DR HSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 108
FT NON_TER 108
SEQUENCE 108 AA: 11633 MW; 87BEDC3E41FCCA37 CRC64;

Query Match 63.6%; Score 360; DB 4; Length 108;
Best Local Similarity 63.6%; Pred. No. 3.7e-32;
Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKPMSTVGVDRVSTICKASQDVTADVQYQKQSPKLLIYASTRTHTGVPD 60
Db 1 DIVMTQSHKPMSTVGVDRVSTICKASQDVTADVQYQKQSPKLLIYASTRTHTGVPD 60

RESULT 5
Q9ULB3
ID Q9ULB3 PRELIMINARY: PRT: 108 AA.
AC Q9ULB3: 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

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DR HSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR SMART: SM00406; IgV_1.
FT NON_TER 108
FT NON_TER 108
SEQUENCE 108 AA: 11787 MW; DB5845F19724F84E CRC64;

Query Match 63.4%; Score 361; DB 4; Length 108;
Best Local Similarity 62.6%; Pred. No. 2.8e-32;
Matches 68; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKPMSTVGVDRVSTICKASQDVTADVQYQKQSPKLLIYASTRTHTGVPD 60
Db 1 DIVMTQSHKPMSTVGVDRVSTICKASQDVTADVQYQKQSPKLLIYASTRTHTGVPD 60

RESULT 4
Q9ULJ70
ID Q9ULJ70 PRELIMINARY: PRT: 108 AA.
AC Q9ULJ70: 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC [11_TaxID=9606;
RN [11_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA Myosin-reactive autoantibodies in rheumatic carditis and normal
RA (Fragment).
DR EMBL: AF035044; RAD56280.1; -.
DR HSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 108
FT NON_TER 108
SEQUENCE 108 AA: 11633 MW; 87BEDC3E41FCCA37 CRC64;

Query Match 63.3%; Score 360; DB 4; Length 108;
Best Local Similarity 63.3%; Pred. No. 3.7e-32;
Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKPMSTVGVDRVSTICKASQDVTADVQYQKQSPKLLIYASTRTHTGVPD 60
Db 1 DIVMTQSHKPMSTVGVDRVSTICKASQDVTADVQYQKQSPKLLIYASTRTHTGVPD 60

RESULT 5
Q9ULB3
ID Q9ULB3 PRELIMINARY: PRT: 108 AA.
AC Q9ULB3: 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

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Q8R062					PRT; 234 AA.
ID	Q8R062				PRELIMINARY;
AC	Q8R062:				
DC	01-JUN-2002	(TrEMBLrel. 21, Created)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)			
DF	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)			
DZ	Hypothetical protein Y_9748				
OC	Karyophilin-like cytoplasmic protein.				
OE	Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OF	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;				
OX	NCBI_TaxID=10090;				
RN	[1]				SEQUENCE FROM N.A.
RP					RESEARCH COLOR;
RL					STATUS;
RI					Submitted (APR-2002) to the EMBL/GenBank/DDAJ databases.

[illegible]

	81.	RFSGSGTHSYLSINLEPDIATTCQTSOFFPFPGSGRKLEIK	147
DD			
		RESULT 11	
		Q91WF8	
	AC	Q91WF8	PREDIMINARY; PRT: 234 AA.
	ID	Q91WF8	
	CD	Q91WF8	
	DT	01-DEC-2001	(TREMblrel_19, Created)
	DT	01-DEC-2001	(TREMblrel_19, Last sequence update)
	DT	01-DEC-2001	(TREMblrel_19, Last annotation update)
	DE	Hypothetical 25.9 kDa protei..	
	OS	Mus musculus (Mouse).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	
	NCBI_TaxID=10090;		
	ON	[1]	DENANCE FROM N.A.
	RP	SEQUENCE NOT REFINED	
	RA	Strausberg R.;	
	RL	Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.	
	EMBL:	BC015292; AAIH51292.1; -	
	InterPro:	IPR003006; I9_MKC.	
	DR	InterPro: IPR001865; Ribosomal_S2.	
	DR	plan; PF00047; I9; 2.	
	DR	PROSITE: PS00390; IG_MKC; UNKNOWN_1	
	DR	PSD00390; Ribosomal_S2_1; UNKNOWN_1.	
	KW	Hypothetical protein	
	SQ	SEQUENCE 234 AA: 25929 MW: 80080565g781202 CRC64:	

[illegible]

RESULT 12

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ID Q0UL77 PRELIMINARY; PRT: 108 AA.
AC AC Q0UL77:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-DEC-2001 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=827139; PubMed=9614934;
RA Kuhlmann B., Van der Merwe F.L.M., Kalis N.N., Berney S.M.,
RA Young D.C.:
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF350373; AAD56273.1; -.
DR HSPG: P01607; RGI.
DR InterPro: IPR003596; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGv_1.
FT NON_TER 1
FT TER 108
SQ SEQUENCE 108 AA; 11738 MW; C0668176CAD16F3 CRC64;
Query Match
Best Local Similarity 59.8%; Score 340; DB 4; Length 108;
Matches 64; Conservative 19; Mismatches 24; Indels 0; Gaps 0;
QY 1 DIVMTQSKHFKSTSGVSDRVTICAKSDQGVGYAVDWXQKPSGLILYYWASTRTGTGVPD 60
DY ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
DY 1 DIPTQTSFSLSSASVDKRVITICRAGSYSSLYMNYQKPAPNLIYYAASSLSQGPS 60
QY 61 DTFGSGSGTDFLTINVOSEDLAFQGVQNYLPFGAGTWLDLK 107
DY ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
DY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCQQSYSTSWTGEGTKVEIK 107

RESULT 13
Q06PF6 PRELIMINARY; PRT: 116 AA.
AC Q06PF6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE kappa 1 light chain variable region (Fragment).
DS DNKL.
GN Homo sapiens (Human)
OS Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RA "The tropism of organ involvement in primary systemic amyloidosis:
RT correlation of Ig (V) germ line gene use and clonal plasma cell
RL burden.";
RL Blood 98:714-720(2001).
DR EMBL: AF361758; AKN51465.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
FT NON_TER 116
FT TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFC57 CRC64;
Query Match
Best Local Similarity 59.8%; Score 340; DB 4; Length 116;

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DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FW Hypothetical protein.
FW Name: 1
FW NCBI: 233 AA; 25781 MW; BIC184DA149A16EB CRC64;
SQ SEQUENCE

Query Match 58.9%; Score 335; DB 11; Length 233;
Best Local Similarity 56.1%; Pred. NO. 5.5e-29;
Matches 60; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

Oy 1 DIWVQSHKFMSTVSQDYSICKASQDVGTAVDWYQKPCQSPKLLIYWASTRHTGVDP 60
|||
Db 20 DIQMTQTSSLSASLGDRVTISCSGSGIANYLNNYQKPDGTALLIYYTSSLSGQVPS 79
|||
Oy 61 RFTSGSGTDFTLTITNWQSEDLADYFCQYNSYPLTFGAGTMLDLK 107
|||
Db 80 RFSGSGTDYSLTISNLEPEDIATYCCQYRYLPMTFGGKLEIK 126
|||

Search completed: July 21, 2003, 13:35:08
Job time : 48.2342 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 21, 2003, 13:32:31 ; Search time 34.7072 Seconds
(without alignments)
393.303 Million cell updates/sec

Title: US-09-929-546-8
Perfect score: 619
Sequence: 1 EVOLQSGPELVKPGTISR.....CAAGWFDYWGQGTTLTVSS 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 11875970 residues
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep1.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep2.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	619	100.0	115	US-09-929-546-8	Sequence 8, Appl
2	619	100.0	115	US-09-929-546-8	Sequence 8, Appl
3	619	100.0	115	US-09-929-546-8	Sequence 8, Appl
4	619	100.0	130	US-09-929-546-4	Sequence 4, Appl
5	496	80.1	117	US-09-956-206A-76	Sequence 76, Appl
6	496	80.1	136	US-09-956-206A-47	Sequence 2, Appl
7	493.5	79.7	232	US-09-754-998-2	Sequence 47, Appl
8	492	79.5	118	US-09-802-093-5	Sequence 2, Appl
9	492	79.5	118	US-09-802-093-5	Sequence 5, Appl
10	492	79.5	125	US-09-929-546-20	Sequence 8, Appl
11	491	79.3	125	US-09-929-546-20	Sequence 20, Appl
12	486.5	78.5	672	US-09-900-766-1	Sequence 1, Appl
13	485	78.4	119	US-09-811-123-1	Sequence 1, Appl
14	485	78.4	119	US-09-811-123-1	Sequence 1, Appl
15	484	78.2	132	US-09-982-501-2	Sequence 14, Appl
16	484	78.2	569	US-09-807-721-2	Sequence 2, Appl

17	480.5	77.6	601	11	US-09-480-236-1	Sequence 1, Appl
18	478	77.2	152	10	US-09-881-823-20	Sequence 20, Appl
19	472.5	76.3	111	15	US-10-032-482-5	Sequence 5, Appl
20	472.5	76.3	111	15	US-10-032-482-5	Sequence 5, Appl
21	472.5	76.3	111	15	US-10-032-482-5	Sequence 5, Appl
22	466	75.3	130	10	US-09-839-447A-3	Sequence 3, Appl
23	466	75.3	130	10	US-09-839-447A-3	Sequence 3, Appl
24	466	75.3	130	10	US-10-153-271-3	Sequence 3, Appl
25	466	75.3	438	11	US-09-903-327A-6	Sequence 6, Appl
26	466	75.3	438	11	US-09-903-327A-6	Sequence 6, Appl
27	466	75.3	438	11	US-09-903-327A-6	Sequence 6, Appl
28	466	75.3	438	11	US-09-903-327A-12	Sequence 12, Appl
29	466	75.3	438	11	US-09-903-327A-12	Sequence 12, Appl
30	465	75.1	113	11	US-09-924-059-2	Sequence 2, Appl
31	465	75.1	113	11	US-09-924-059-2	Sequence 2, Appl
32	465	75.1	237	11	US-09-924-059-9	Sequence 9, Appl
33	464.5	75.0	274	10	US-09-924-059-9	Sequence 10, Appl
34	464.5	75.0	274	10	US-09-924-059-9	Sequence 10, Appl
35	462.5	74.7	259	15	US-09-813-659-30	Sequence 30, Appl
36	462.5	74.7	259	15	US-09-813-659-30	Sequence 30, Appl
37	462.5	74.7	259	15	US-10-207-655-13	Sequence 13, Appl
38	459	74.2	117	11	US-09-956-206A-78	Sequence 78, Appl
39	459	74.2	117	11	US-09-956-206A-78	Sequence 78, Appl
40	459	74.2	136	11	US-09-956-206A-63	Sequence 63, Appl
41	458	74.0	142	10	US-09-772-120-8	Sequence 8, Appl
42	458	74.0	119	12	US-09-795-515-30	Sequence 30, Appl
43	458	74.0	119	12	US-10-267-286A-10	Sequence 10, Appl
44	457.5	73.9	152	12	US-09-795-515-7	Sequence 7, Appl
45	457.5	73.9	152	12	US-09-795-515-7	Sequence 7, Appl
46	457.5	73.9	152	12	US-09-540-478-14	Sequence 14, Appl
47	457.5	73.9	152	12	US-09-540-478-14	Sequence 14, Appl
48	457.5	73.9	152	12	US-10-036-246-10	Sequence 10, Appl
49	457.5	73.9	152	12	US-10-036-246-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-929-546-8
Sequence 8, Application US/09929665
Publication No. US2003003101A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: Lois M. Kwasigroch; BZL 242/024
CURRENT APPLICATION NUMBER: 09/099299, 665
PRIORITY CLAIMING DATE: 09/09/99
PRIOR APPLICATION NUMBER: 09/4357,704
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 115
TYPE: PRT
ORGANISM: Mus sp.
US-09-929-665-8

Query Match 100.0% Score 619; DB 12; Length 115;
Best Local Similarity 100.0% Pred. No. 5,2e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVOLQSGPELVKPGTISRICKSTSYTFTYTHHWKQSGLKSLMIGNPNNGTTY 60
DB 1 EVOLQSGPELVKPGTISRICKSTSYTFTYTHHWKQSGLKSLMIGNPNNGTTY 60
OY 61 NOKPEDKATLVOKSSSTAYMELKSLTSDSAYVYCAAGWFDYWGQGTTLTVSS 115
DB 61 NOKPEDKATLVOKSSSTAYMELKSLTSDSAYVYCAAGWFDYWGQGTTLTVSS 115

```

RESULT 2
US-09-929-546-8
: Application US/09929546
: Publication No. US20030031673A1
: GENERAL INFORMATION:
: APPLICANT: Bander, Neil H.
: TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
: FILE REFERENCE: Lois M. Kwasigroch: B2L 242/028
: CURRENT APPLICATION NUMBER: US/09/929,546
: CURRENT FILING DATE: 2001-08-13
: PRIOR FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: US 08/838,682
: PRIOR FILING DATE: 1997-04-09
: PRIOR APPLICATION NUMBER: US 60/016,976
: PRIOR FILING DATE: 1996-05-06
: PRIOR APPLICATION NUMBER: US 60/022,125
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 8
: LENGTH: 115
: TYPE: PRT
: ORGANISM: Mus sp.
:
US-09-929-546-8
Query Match 100.0% Score 619; DB 12; Length 115;
Best Local Similarity 100.0% Pred. No. 5,2e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPTSVRISCKTSYTFYTHVVKQSHKSGLEWGNPNNGTGY 60
Db 1 EVLOQSGPELVKPTSVRISCKTSYTFYTHVVKQSHKSGLEWGNPNNGTGY 60
QY 61 NOKFEDKATLVDKSSSTAYMELRSLTSEDSAVTYCAAGNFYWGOGTTLTVSS 115
Db 61 NOKFEDKATLVDKSSSTAYMELRSLTSEDSAVTYCAAGNFYWGOGTTLTVSS 115

RESULT 3
US-09-929-665-4
: Application US/09929665
: Publication No. US2003003101A1
: GENERAL INFORMATION:
: APPLICANT: Bander, Neil H.
: TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: Lois M. Kwasigroch: B2L 242/024
: CURRENT APPLICATION NUMBER: US/09/929,665
: CURRENT FILING DATE: 2001-08-13
: PRIOR FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: US 08/838,682
: PRIOR FILING DATE: 1997-04-09
: PRIOR APPLICATION NUMBER: US 60/016,976
: PRIOR FILING DATE: 1996-05-06
: PRIOR APPLICATION NUMBER: US 60/022,125
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 130
: TYPE: PRT
: ORGANISM: Mus sp.
:
US-09-929-665-4
Query Match 100.0% Score 619; DB 12; Length 130;
Best Local Similarity 100.0% Pred. No. 5,9e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPTSVRISCKTSYTFYTHVVKQSHKSGLEWGNPNNGTGY 60
Db 1 EVLOQSGPELVKPTSVRISCKTSYTFYTHVVKQSHKSGLEWGNPNNGTGY 60
QY 61 NOKFEDKATLVDKSSSTAYMELRSLTSEDSAVTYCAAGNFYWGOGTTLTVSS 115
Db 61 NOKFEDKATLVDKSSSTAYMELRSLTSEDSAVTYCAAGNFYWGOGTTLTVSS 115

RESULT 4
US-09-929-546-4
: Application US/09929546
: Publication No. US20030031673A1
: GENERAL INFORMATION:
: APPLICANT: Bander, Neil H.
: TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
: FILE REFERENCE: Lois M. Kwasigroch: B2L 242/028
: CURRENT APPLICATION NUMBER: US/09/929,546
: CURRENT FILING DATE: 2001-08-13
: PRIOR FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: US 08/838,682
: PRIOR FILING DATE: 1997-04-09
: PRIOR APPLICATION NUMBER: US 60/016,976
: PRIOR FILING DATE: 1996-05-06
: PRIOR APPLICATION NUMBER: US 60/022,125
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 130
: TYPE: PRT
: ORGANISM: Mus sp.
:
US-09-929-546-4
Query Match 100.0% Score 619; DB 12; Length 130;
Best Local Similarity 100.0% Pred. No. 5,9e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPTSVRISCKTSYTFYTHVVKQSHKSGLEWGNPNNGTGY 60
Db 1 EVLOQSGPELVKPTSVRISCKTSYTFYTHVVKQSHKSGLEWGNPNNGTGY 70
QY 61 NOKFEDKATLVDKSSSTAYMELRSLTSEDSAVTYCAAGNFYWGOGTTLTVSS 115
Db 61 NOKFEDKATLVDKSSSTAYMELRSLTSEDSAVTYCAAGNFYWGOGTTLTVSS 125

RESULT 5
US-09-956-206A-76
: Sequence 76, Application US/09956206A
: Patent No. US20020164339A1
: GENERAL INFORMATION:
: APPLICANT: CERTANT, ROBERTO J.R.
: PETERSON, JERRY A.
: TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
: M3 ANTI-BM46 ANTIBODY, METHODS OF USE THEREOF, AND
: METHODS OF HUMANIZING ANTIBODY PEPTIDES
:
NUMBER OF SEQUENCES: 81
: CORRESPONDING AMINO ACID SEQUENCE:
: ADDRESSES: MORRISON & FORESTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: FILE NAME: 0956206A.rapb
: COMPUTER: IBM PC, compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/956,206A
: FILING DATE: 19-Apr-2002
: CLASSIFICATION: G06K9/00
: PRIOR APPLICATION DATA:
:

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: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 118
: TYPE: PRT
: ORGANISM: Mus musculus
: US-10-165-732A-5

Query Match
  Local Similarity 79.5% Score 492; DB 15; Length 118;
  Matches 93; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

Qy 1 EVLQAQSGPELVKPGFTSVRIKSCKTSQYTFTEVTIIRHWKQSHGKSLKLEIKNIPNNGCTT 60
Db 1 EVLQAQSGPELVKPGASVYKIPCKASGYTFTEYNDMWYKQSHGKSLKLEIKNIPNNGCTT 60
Qy 61 NQKFEKATLVTKDSSSTAYWELSLTSDSNAVYCA--CWNPYMGQCTTLTVSS 115
Db 61 NQKFEKATLVTKDSSSTAYWELSLTSDTAVYFCARDHYDYFQMGQCTTLTVSS 117

RESULT 10
: US-09-929-665-20
: Sequence 20, Application US/09929665
: Publication No. US2003003101A1
: GENE: PROSTATE CANCER; LOC: 10q36
: APPLICANT: Bandner, Neil H.
: TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: Lois M. Kwasiroch; BZL 242,024
: CURRENT APPLICATION NUMBER: US/09/929,665
: CURRENT FILING DATE: 2001-08-13
: PRIOR APPLICATION NUMBER: 09/317,704
: PRIOR FILING DATE: 1999-07-20
: PRIOR PUBLICATION NO.: 2001/08/938,582
: PRIOR FILING DATE: 1997-04-09
: PRIOR APPLICATION NUMBER: US 60/016,976
: PRIOR FILING DATE: 1996-05-06
: PRIOR APPLICATION NUMBER: US 60/022,125
: PRIOR FILING DATE: 1996-07-18
: NUMBER OF SEQ ID NOS: 21
: CROSS-REFERENCE TO PATENTIN version 3.0
: SEQ ID NO 20
: LENGTH: 125
: TYPE: PRT
: ORGANISM: Mus sp.
: US-09-929-665-20

Query Match
  Local Similarity 79.5% Score 491; DB 12; Length 125;
  Matches 96; Conservative 10; Mismatches 9; Indels 10; Gaps 2;

Qy 1 EVLQAQSGPELVKPGFTSVRIKSCKTSQYTFTEVTIIRHWKQSHGKSLKLEIKNIPNNGCTT 59
Db 1 EVLQAQSGPELVKPGASVYKISCKASGYTFTEYTDYIMNHWKQSPKSLKLEIKNIPNGGTS 60
Qy 60 NQKFEKATLVTKDSSSTAYWELSLTSDSNAVYCAAG-----WNPYMGQCTT 110
Db 61 NQKFEKATLVTKDSSSTAYWELSLTSDSNAVYCAAGYVSSYWAYYAFDYGQCTT 120

Qy 111 LTVSS 115
Db 121 VTVSS 125

RESULT 11
: US-09-929-546-20
: Sequence 20, Application US/09929546
: Publication No. US20030031673A1
: GENE: PROSTATE CANCER; LOC: 12p36
: APPLICANT: Bandner, Neil H.
: TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
: FILE REFERENCE: Lois M. Kwasiroch; BZL 242,028
: CURRENT APPLICATION NUMBER: US/09/929,546
: CURRENT FILING DATE: 2001-08-13

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; PRIOR APPLICATION NUMBER: 09/37,708
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 08/938,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus sp.
;
US-09-929-546-20

Query Match
Best Local Similarity 76.6%; Score 491; DB 12; Length 125;
Matches 96; Conservative 10; Mismatches 9; Indels 10; Gaps 2;

OY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 59
DB 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 59
OY 60 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 110
DB 61 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 120
OY 111 LTVSS 115
DB 121 VTVSS 125

RESULT 12
US-09-900-766-1
; Sequence 1. Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ERLANDSSON, PER
; APPLICANT: NORDSTRAND, NIKOLAJ
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match
Best Local Similarity 78.6%; Score 486.5; DB 12; Length 672;
Matches 93; Conservative 9; Mismatches 13; Indels 5; Gaps 1;

OY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 60
DB 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 60
OY 61 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 115
DB 61 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 120

RESULT 13
US-09-811-123-1
; Sequence 1. Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Rickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811.123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-1

Query Match
Best Local Similarity 78.4%; Score 485; DB 10; Length 119;
Matches 90; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

OY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 60
DB 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 60
OY 61 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 115
DB 61 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 119

RESULT 14
US-10-268-501-2
; Sequence 2. Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Sliwowski, Mark X
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: PI467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-268-501-2

Query Match
Best Local Similarity 75.6%; Score 485; DB 15; Length 119;
Matches 90; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

OY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 60
DB 1 EVLOQSGPELVKPGTSVRISCKTSGYTFETTHHWKSHGKSLKLEININPANGGTT 60
OY 61 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 115
DB 61 NQKFDKATLTVDKSSSTAYMELASLTSDSAVYCA-----AGNFDYWGQGT 119

RESULT 15
US-09-811-123-1
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US-09-982-107-14
: Sequence 14, Application US/09982107
: Patent No. US2002015958A1
: INVENTOR: GUY, GUY, ANDREW C.
: APPLICANT: HAITI
: APPLICANT: HEIN, MICH B.
: TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
: FILE REFERENCE: EPI3002E
: CURRENT APPLICATION NUMBER: US/09/982.107
: CURRENT FILING DATE: 2001-10-16
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: SeqEdit Ver. 2.1
: SEQ ID NO 14
: LENGTH: 132
: TYPE: PRT
: ORGANISM: Unknown Organism
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Gamma 1
US-09-982-107-14

Query Match      78.2%  Score 484;  DB 11;  Length 132;
Best Local Similarity 81.6%  Pred. No. 5.9e-36;
Matches 93;  Conservative 7;  Mismatches 12;  Indels 2;  Gaps 1;

Oy      2  VOLQSGPELVKPGTSVRISCKTSGYTFETTHRWKSHQSKLEWIGNINPNNGGTTYN 61
Db      21  VOLQSGPELVKPGTSVRISCKASGTFTHRWKSHQSKLEWIGTFPNNGGTTYN 80
Oy      62  QKFEDKATLVYDKSSSTAYMELASLTSEDSAVTYCAAGNFDYNGOGTTLTVSS 115
Db      81  QKFENKATLVVNSSTSTAYMELASLTSEDSAVTYCAT--YFDYNGOGTTLTVSS 132

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Search completed: July 21, 2003, 13:46:33
Job time : 35.7072 secs

SUMMARIES									
Result No.	Score	Query Match	Length	DB	ID	Description			
1	539.5	87.2	128	2	I37267	Ig	heavy	chain	V r
2	512.5	82.6	128	2	I37267	Ig	heavy	chain	V r
3	511.5	82.6	128	2	I37267	Ig	heavy	chain	V r
4	512	82.7	121	2	I37266	Ig	heavy	chain	V r
5	510.5	82.5	113	2	I35535	Ig	heavy	chain	V r
6	508.5	82.1	118	1	IHMMS38	Ig	heavy	chain	V r
7	505	81.6	117	1	IHMMS4E	Ig	heavy	chain	V r
8	505	81.6	117	1	IHMMSJ5	Ig	heavy	chain	V r
9	505	81.6	140	2	I701407	Ig	heavy	chain	V r
10	503.5	81.0	123	2	I37266	Ig	heavy	chain	V r
11	501.5	81.0	123	2	I37266	Ig	heavy	chain	V r
12	496	80.9	121	2	I37266	Ig	heavy	chain	V r
13	494.5	79.9	112	2	I509597	Ig	heavy	chain	V-D
14	491.5	79.4	113	2	I355333	Ig	heavy	chain	V r
15	490.5	79.2	137	2	I325131	Ig	heavy	chain	pre
16	489	79.0	151	2	IPL0011	Ig	heavy	chain	pre
17	488.5	78.9	113	2	I355228	Ig	heavy	chain	V r
18	488.5	78.6	113	2	I355228	Ig	heavy	chain	V r
19	486.5	78.6	113	2	I355333	Ig	heavy	chain	V r
20	483.5	78.1	113	2	I355332	Ig	heavy	chain	V r
21	476.5	77.0	122	2	IPI0887	Ig	heavy	chain	V r
22	475.5	76.8	139	2	I327609	Ig	heavy	chain	pre
23	475	76.7	125	2	I3PH0100	Ig	heavy	chain	V r
24	474	76.6	114	2	I320710	Ig	heavy	chain	V r
25	473.5	76.5	119	2	I3F0502	Ig	heavy	chain	V r
26	471.5	76.2	127	2	I349382	Ig	heavy	chain	V r
27	471	76.1	129	2	I349382	Ig	heavy	chain	V r
28	469.5	75.8	150	2	I3PH0445	Ig	heavy	chain	V r
29	468.5	75.7	135	2	I3PH0057	Ig	heavy	chain	pre

RESULT 5

RESULT 3

A:ResIdues: 1-128 <RUF>

Qy

ig heavy

F: 19-100

1 EVQLQQSGPELVKPGASVKISCKASGYTF^{TD}YYMNWVKQSHGKSL^{EW}IGDINPNNGTSY 60

A;Accession: E37267

A:Status: Preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-112 <R0>
 C:Species: Mus musculus (house mouse)
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:19-102/Domain: immunoglobulin homology <IM>

Query Match 81.0% Score 501.5; DB 2; Length 122;
 Best Local Similarity 82.1%; Pred. No. 5; 3e-37;
 Matches 96; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

Qy 2 VOLQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTTY 61
 Db 6 VOLQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTTNN 65

Qy 62 QKFEDKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 115
 Db 66 QKRFKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 122

RESULT 12

H37266

Ig heavy chain V region (PV54) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Oct-1991 #sequence_revision 12; Indels 3; Gaps 1;

A:Accession: H37266 Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Mol. Biol. 267: 660-663, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-

A:Reference number: A38740; MUID:91177923; PMID:1706720

A:Accession: H37266

A:Status: Preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-112 <R0>

C:Species: Mus musculus (house mouse)

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:19-100/Domain: immunoglobulin homology <IM>

Query Match 80.1% Score 496; DB 2; Length 121;
 Best Local Similarity 83.9%; Pred. No. 9; 3e-37;
 Matches 99; Conservative 3; Mismatches 10; Indels 5; Gaps 2;

Qy 2 VOLQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTTY 61
 Db 6 VOLQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTY -N 63

Qy 62 QKFEDKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 115
 Db 64 QKRFKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 121

RESULT 13

S09957

Ig heavy chain V-D-J region (106-10E) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12; Indels 3; Gaps 1;

A:Accession: S09957 Ishaq, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izul, S.

Eur. J. Immunol. 20: 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies

A:Reference number: S09955; MUID:90269328; PMID:2347362

A:Accession: S09957

A:Molecule type: mRNA

A:Residues: 1-112 <R0>

C:Species: Mus musculus (house mouse)

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IM>

Query Match 79.9% Score 494.5; DB 2; Length 112;
 Best Local Similarity 80.9%; Pred. No. 1; 2e-36;
 Matches 93; Conservative 10; Mismatches 9; Indels 3; Gaps 1;

Qy 1 EVLOQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTTY 60
 Db 1 EVLOQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTYST 60
 Qy 61 NQKFEKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 115
 Db 61 NQKFEKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 112

RESULT 14

S55533

Ig heavy chain V region pe26 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C:Accession: S55533

J. Mol. Biol. 247: 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies u-

A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55533

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <R0>

C:Species: Mus musculus (house mouse)

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IM>

Query Match 79.4% Score 491.5; DB 2; Length 113;
 Best Local Similarity 82.5%; Pred. No. 2; 1e-36;
 Matches 94; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Qy 2 VOLQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTTY 61
 Db 1 VOLQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTY 60

Qy 62 QKFEDKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 115
 Db 61 QKRFKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 113

RESULT 15

H32513

Ig heavy chain precursor V region (BXW16) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

A:Accession: H32513

R. Kofler, R.; Ströbel, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.

Cell. Invest. 82: 857-860, 1988

A:Title: Heavy chain variable region chain variable region gene complex organization a

A:Reference number: A94689; MUID:88331394; PMID:3136286

A:Accession: H32513

A:Molecule type: DNA

A:Residues: 1-137 <R0>

C:Species: Mus musculus (house mouse)

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IM>

Query Match 79.2% Score 490.5; DB 2; Length 137;
 Best Local Similarity 79.7%; Pred. No. 3; 2e-36;
 Matches 95; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

Qy 1 EVLOQSGPELVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTTY 60
 Db 20 EIQQQSGAEIVKPGTSVRISCKTSQYFTFTYTHHWKSHGKSLKLEWIGNPNNGGTYST 79

Qy 61 NQKFEKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 115
 Db 80 NQKFEKATLVTKSSSTAYMELRSLSSEDSAVVYCAAGNFDYWGOGTTLTVSS 137

Search completed: July 21, 2003, 13:33:21
Job time : 26.3829 secs

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Result	No.	Score	Query	Match	Length	DB	ID	Description
1	508.5	82.1	118	1	HV51_MOUSE	P06330	mus musculus	
2	505	81.6	117	1	HV12_MOUSE	P01756	mus musculus	
3	505	81.6	117	1	HV13_MOUSE	P01757	mus musculus	
4	457.5	73.9	139	1	HV07_MOUSE	P01751	mus musculus	
5	455.1	72.9	136	1	HV15_MOUSE	P01755	mus musculus	
6	444	71.7	120	1	HV03_MOUSE	P01747	mus musculus	
7	441	71.2	140	1	HV02_MOUSE	P01746	mus musculus	
8	438	70.8	117	1	HV14_MOUSE	P01758	mus musculus	
9	423.5	68.4	120	1	HV50_MOUSE	P03929	mus musculus	
10	417	67.4	138	1	HV04_MOUSE	P03980	mus musculus	
11	402	64.9	117	1	HV04_MOUSE	P01748	mus musculus	
12	397	64.5	117	1	HV09_MOUSE	P01745	mus musculus	
13	397	64.5	117	1	HV09_MOUSE	P01746	mus musculus	
14	397	64.1	117	1	HV49_MOUSE	P06328	mus musculus	
15	387	62.5	117	1	HV10_MOUSE	P01754	mus musculus	
16	385	62.2	117	1	HV06_MOUSE	P01750	mus musculus	
17	382.5	61.8	147	1	HV1C_HUMAN	P01744	homo sapien	
18	382	61.7	117	1	HV05_MOUSE	P01749	mus musculus	
19	382	61.7	117	1	HV52_MOUSE	P06327	mus musculus	
20	374	60.4	117	1	HV1C_HUMAN	P23083	homo sapien	
21	336	54.3	117	1	HV1C_HUMAN	P01743	homo sapien	
22	336	54.3	117	1	HV1C_HUMAN	P01743	homo sapien	
23	324.5	52.4	116	1	HV00_MOUSE	P01743	homo sapien	
24	309	49.9	125	1	HV1F_HUMAN	P06326	homo sapien	
25	306	49.4	117	1	HV1D_MOUSE	P01811	mus musculus	
26	302.5	48.9	124	1	HV1D_HUMAN	P01760	homo sapien	
27	302	48.8	117	1	HV1A_HUMAN	P01742	homo sapien	
28	302	48.8	121	1	HV3J_HUMAN	P01771	homo sapien	
29	299.5	48.4	124	1	HV1E_HUMAN	P01761	homo sapien	
30	297.9	48.1	120	1	HV1E_HUMAN	P01782	homo sapien	
31	295.5	47.7	119	1	HV1E_HUMAN	P01803	homo sapien	
32	295.5	47.7	119	1	HV1E_HUMAN	P01803	homo sapien	
33	295.5	47.7	120	1	HV1E_HUMAN	P08423	homo sapien	

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 EN [1]_TaxID=10090;
 RX SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RP MEDLINE=83075344; PubMed=6816276;
 RA Kerry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains";
 RT J Biol Chem 264(1989):11111-11115;
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC PROTEIN WAS ALSO BEING DETERMINED.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC PTR; A202039; MH64E.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR003006; Ig-MHC.
 DR InterPro; IPR003596; Ig-LV.
 DR Pfam; P00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region; Glycoprotein.
 FT DISULFID 22 96 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
 Query Match 81.6%; Score 505; DB 1; Length 117;
 Best Local Similarity 81.2%; Pred. No. 2-le-42;
 Matches 95; Conservative 11; Mismatches 11; Indels 2; Gaps 1;
 Qy 1 EVLOQSGPELVKPTGVSRISCKTSYFTFTHVVKQSHGKSLWIGNIPNNGTGY 60
 Db 1 EVLOQSGPELVKPTGVSRISCKTSYFTFTHVVKQSHGKSLWIGNIPNNGTGY 60
 Qy 61 NOKFKGKATLVOKSSSTAYMLRSLTSSEDSAVYICAG--GNPKYQGGTTLTVSS 115
 Db 61 NOKFKGKATLVOKSSSTAYMLRSLTSSEDSAVYICAG--GNPKYQGGTTLTVSS 115
 Qy 61 NOKFKGKATLVOKSSSTAYMLRSLTSSEDSAVYICAG--GNPKYQGGTTLTVSS 115
 Db 61 NOKFKGKATLVOKSSSTAYMLRSLTSSEDSAVYICAG--GNPKYQGGTTLTVSS 115
 RESULT 3
 TR1358P
 AC P01752; STANDARD; PRT; 117 AA.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Ig heavy chain v region J558.
 DE Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 EN [1]_TaxID=10090;
 RX SEQUENCE.
 RP MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain v-region gene segments";
 RT J Biol Chem 264(1989):11111-11115;
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC PTR; A26242; MH65S.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR003006; Ig-MHC.
 DR InterPro; IPR003596; Ig-LV.
 DR Pfam; P00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13024 MW; 29E2AF4BE447E41 CRC64;
 Query Match 81.6%; Score 505; DB 1; Length 117;
 Best Local Similarity 81.2%; Pred. No. 1-le-37;
 Matches 87; Conservative 10; Mismatches 18; Indels 5; Gaps 1;

Best Local Similarity 81.2%; Pred. No. 2-le-42;
 Matches 95; Conservative 11; Mismatches 11; Indels 2; Gaps 1;
 Qy 1 EVLOQSGPELVKPTGVSRISCKTSYFTFTHVVKQSHGKSLWIGNIPNNGTGY 60
 Db 1 EVLOQSGPELVKPTGVSRISCKTSYFTFTHVVKQSHGKSLWIGNIPNNGTGY 60
 Qy 61 NOKFKGKATLVOKSSSTAYMLRSLTSSEDSAVYICAG--GNPKYQGGTTLTVSS 115
 Db 61 NOKFKGKATLVOKSSSTAYMLRSLTSSEDSAVYICAG--GNPKYQGGTTLTVSS 117
 RESULT 4
 HV07_MOUSE
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain v region BI-8/186-2 precursor.
 DE Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 EN NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8171548; PubMed=6788376;
 RA Bethwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RT Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
 CC CELL.
 CC -1- MISCELLANEOUS: RES TO THE RAPTEIN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
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 CC or send an email to license@isb-sb.ch.
 CC -----
 CC EMBL; J00529; AAA38170.1;
 DR PIR; A02034; MH6S18.
 DR HSP; P01810; 2F53.
 DR InterPro; IPR003006; Ig-MHC.
 DR InterPro; IPR003596; Ig-LV.
 DR Pfam; P00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 139
 FT DOMAIN 20 49 IG HEAVY CHAIN V REGION BI-8/186-2.
 FT DOMAIN 20 49 FRAMWORK-1.
 FT DOMAIN 50 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 50 58 FRAMWORK-2.
 FT DOMAIN 86 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMWORK-3.
 FT DOMAIN 118 124 D SEGMENT.
 FT DOMAIN 125 139 JH2 SEGMENT.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 139 139
 SQ SEQUENCE 139 AA; 13419 MW; 1B57DD4FD0CF465 CRC64;
 Query Match 73.9%; Score 457.5; DB 1; Length 139;
 Best Local Similarity 72.5%; Pred. No. 1-le-37;
 Matches 87; Conservative 10; Mismatches 18; Indels 5; Gaps 1;

Qy 1 EVLOQSGPELVKPTGVSRISCKTSYFTFTHVVKQSHGKSLWIGNIPNNGTGY 60
 Db 20 QVQQLQGNELVDPNSVKLSKASGTFITFTHVVKQKPGNGLEWIGRIDPNSGTRK 79

QY 61 NQKFDKATLVKSSSTAYMELSLTSDSAVYYCA-----AGNFDYWGQGTTLTVSS 115
 DB 80 NENFKSKATLVKSSSTAYMELSLTSDSAVYYCAVYDYSSYFDYWGQGTTLTVSS 139

RESULT 5

HV11_MOUSE STANDARD; PRT; 137 AA.
 AC 201755: 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region S43 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TAXID=10090;
 RN MEDLINE=81234548; PubMed=5788376;
 RX Sequence from N.A.
 RA Batthore D.;
 RA Batthore A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RT "Heavy chain variable region contribution to the NpB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region";
 RL Cell 71:625-637(1991);
 CC "A gamma 2a CHAIN mRNA WAS CLONED FROM A HEBRDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J00539; AAA38172.1; .
 DR PIR: A02038; C2MS43.
 DR HSP; P01810; 2FB0.
 DR InterPro: IPR003596; Ig_MHC.
 DR Pfam: PF00047; Ig_1; Ig_V.
 DR SMART: SM00406; IG; 1.
 DR SIGNAL 1 19
 KW Immunoglobulin V region; Signal.
 FT CHAIN 20 137
 FT SIGNAL 1 19
 FT CHAIN 20 137
 FT NON_TER 136 136
 FT SEQUENCE 137 AA; 13200 MW; ADD5681BF44B8EC9 CRC64;
 Query Match 73.3%; Score 453.5; DB 1; Length 137;
 Best Local Similarity 72.0%; Pred. No. 2.6e-37;
 Matches 85; Conservative 10; Mismatches 20; Indels 3; Gaps 1;
 QY 1 EVLOQSGPELVKPGTSVRISCKTSGYFTFTTHWKSHGKSLKLEINPNNGTTY 60
 DB 20 OVLOQSGPELVKPGTSVRISCKTSGYFTFTTHWKSHGKSLKLEINPNNGTTY 79
 QY 61 NQKFDKATLVKSSSTAYMELSLTSDSAVYYCA---AGNFDYWGQGTTLTVSS 115
 DB 80 NENFKSKATLVKSSSTAYMELSLTSDSAVYYCARLGRYDYWGQGTTLTVSS 137

RESULT 6

HV15_MOUSE STANDARD; PRT; 136 AA.
 AC 201759: 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region BCL1 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TAXID=10090;
 RN MEDLINE=92222262; PubMed=6806821;
 RX Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
 RA Blatner F.R.;
 RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
 RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
 RT by two adjacent C_H genes";
 CC EMBL; J00494; AAA38130.1; .
 DR PIR: A02042; HVMS81.
 DR HSP; P01772; 2FB4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00406; IG; 1.
 DR SIGNAL 1 19
 KW Immunoglobulin V region; Signal.
 FT CHAIN 20 136
 FT NON_TER 136 136
 FT SEQUENCE 136 AA; 15078 MW; 6827CF6CDB3F35E CRC64;
 Query Match 72.9%; Score 451; DB 1; Length 136;
 Best Local Similarity 74.4%; Pred. No. 4.5e-37;
 Matches 87; Conservative 11; Mismatches 17; Indels 2; Gaps 1;
 QY 1 EVLOQSGPELVKPGTSVRISCKTSGYFTFTTHWKSHGKSLKLEINPNNGTTY 60
 DB 20 OVLOQSGPELVKPGTSVRISCKTSGYFTFTTHWKSHGKSLKLEINPNNGTTY 79
 QY 61 NQKFDKATLVKSSSTAYMELSLTSDSAVYYCA---GNFDYWGQGTTLTVSS 115
 DB 80 NQKFKATLVKSSSTAYMELSLTSDSANLYCARYGVNFDYWGQGTTLTVSS 136
 RESULT 7
 HV03_MOUSE STANDARD; PRT; 120 AA.
 AC 201747: 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 36-65.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TAXID=10090;
 RN MEDLINE=83131846; PubMed=6186498;
 RX Siskavitz M., Geffer M.L., Brodeur P., Riblet R.,
 RA Marsnak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsonate

Search completed: July 21, 2003, 13:31:53
Job time : 14.4685 secs

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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:29:50 ; Search time 50.7658 Seconds
(without alignments)
466.760 Million cell updates/sec

Title: US-09-929-546-8

perfect score: 619

Sequence: 1 EVQLQQSGPELVKPGTSVRI.....CAAGWNFDYWGGTTLTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Minimum	DB	seq	length:
Maximum	DB	seq	length:

Post-processing: Minimum Match 0%

POST-PROCESSING: MINIMUM MATCH 0%
Maximum Match 100%

Maximum Match 100%
Listing first 45 summaries

Database :

- ```

1: sp.archae:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mmc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Query No. | Score | Match | Length | DB     | ID     | Description  |
|--------|-----------|-------|-------|--------|--------|--------|--------------|
| 1      | 513       | 82.9  | 117   | 11     | 05QXF0 | 05qxf0 | mus musculus |
| 2      | 500       | 80.8  | 117   | 11     | 05QXE9 | 05qxe9 | mus musculus |
| 3      | 487       | 78.7  | 140   | 11     | 0524P8 | 0524p8 | mus musculus |
| 4      | 473.5     | 76.5  | 488   | 11     | 051WR1 | 051wr1 | mus musculus |
| 5      | 473       | 76.4  | 142   | 11     | 0524Q1 | 0524q1 | mus musculus |
| 6      | 464       | 75.0  | 120   | 11     | 052DE8 | 052de8 | mus musculus |
| 7      | 461       | 74.5  | 166   | 11     | 0524E8 | 0524e8 | mus musculus |
| 8      | 460       | 74.3  | 123   | 11     | 05VJ11 | 05vj11 | mus musculus |
| 9      | 459.5     | 74.2  | 145   | 11     | 0524R3 | 0524r3 | mus musculus |
| 10     | 458.5     | 74.1  | 176   | 11     | 0524R6 | 0524r6 | mus musculus |
| 11     | 458       | 74.1  | 141   | 11     | 0524R5 | 0524r5 | mus musculus |
| 12     | 458.5     | 74.1  | 481   | 11     | 0534V5 | 0534v5 | mus musculus |
| 13     | 457.5     | 73.9  | 145   | 11     | 0524Q7 | 0524q7 | mus musculus |
| 14     | 454       | 73.3  | 140   | 11     | 0524R2 | 0524r2 | mus musculus |
| 15     | 453       | 73.2  | 144   | 11     | 0524P5 | 0524p5 | mus musculus |
| 16     | 450.5     | 72.8  | 143   | 11     | 0524R0 | 0524r0 | mus musculus |

## ALIGNMENTS

|                       |                                                                      |              |                        |         |                   |
|-----------------------|----------------------------------------------------------------------|--------------|------------------------|---------|-------------------|
|                       |                                                                      |              |                        |         |                   |
| RESULT 1              |                                                                      |              |                        |         |                   |
| QOQXF0                |                                                                      |              |                        |         |                   |
| ID                    | QOQXF0                                                               | PRELIMINARY: | PRT:                   | 117 AA. |                   |
| AC                    | QOQXF0                                                               |              |                        |         |                   |
| DT                    | 01-MAY-2000 (TReMBLrel. 13, Created)                                 |              |                        |         |                   |
| DT                    | 01-MAY-2000 (TReMBLrel. 13, Last sequence update)                    |              |                        |         |                   |
| DE                    | 01-DEC-2001 (TReMBLrel. 19, Last annotation update)                  |              |                        |         |                   |
| DE                    | Immunoglobulin heavy chain V-D-J region [fragment].                  |              |                        |         |                   |
| OC                    | Mus musculus (Mouse), Bordsata: Granulata; Vertebrata; Euteleostomi; |              |                        |         |                   |
| CC                    | Mammalia; Euteleostei, Rodentia; Sciurognathi; Muridae; Mus.         |              |                        |         |                   |
| NCBI_TaxId=10090;     |                                                                      |              |                        |         |                   |
| [1]                   | SEQUENCE FROM N.A.                                                   |              |                        |         |                   |
| RP                    | Clemens A., Rademackers A., Specht C., Koelsch E.;                   |              |                        |         |                   |
| RL                    | Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases .            |              |                        |         |                   |
| RL                    | EMBL; AJ225171; CAB65236.1; -                                        |              |                        |         |                   |
| DR                    | HSSP; P01789; INCP.                                                  |              |                        |         |                   |
| DR                    | InterPro; IPR003006; Ig_MHC.                                         |              |                        |         |                   |
| DR                    | SMART; SM00047; Ig_V.                                                |              |                        |         |                   |
| DR                    | Pfam; PF00047; Ig_1.                                                 |              |                        |         |                   |
| DR                    | SMART; SM00406; IGv; 1.                                              |              |                        |         |                   |
| FT                    | NON_TER                                                              | 1            | NON_TER                | 1       |                   |
| FT                    | NON_TER                                                              | 117          | NON_TER                | 117     |                   |
| SQ                    | SEQUENCE                                                             | 117 AA;      | D816AD058A47E4C CRC54; |         |                   |
| Query Match           |                                                                      |              |                        |         |                   |
| Best local Similarity |                                                                      | 82.9%;       | Score 513;             | DB 11;  | Length 117%.      |
| Matches               |                                                                      | 97;          | Conservative           | 97;     | Indels 2; Gaps 1; |
| Oy                    | 1 EVOLQGSGPELVKPGTSYVRICTSKTSYFFETTHWVKOSHGKSLEIENINPNNGCTTY 60      |              |                        |         |                   |
| Db                    | 1 EVOLQGSGPELVKPGTSYVRICTSKTSYFFETTHWVKOSHGKSLEIENINPNNGCTTY 60      |              |                        |         |                   |

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1 EVQLQDSGPELVKPGTSTVRISCKTSYTFTEYTHVVKQSHCKSLEWIGNINPNNGTTY 60
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1 EVQLQDSGPELVKPGASVKMSCKASYTFDYMKWKVKQSHCKSLEWIGDINPNNGTYSY 60

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[illegible][illegible]



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Db 61 SOKFKKATLVTKSSSTAYMELRSITSDESAVYTCARDYITTYIDBGFAVWGQGLTVT 120
Qy 113 VSS 115
Db 121 VSA 123

RESULT 9
Q924R3 PRELIMINARY: PRT: 145 AA.
AC Q924R3 1
DT 01-DEC-2001 (T:EMBLrel. 19, Created)
DT 01-DEC-2001 (T:EMBLrel. 19, Last sequence update)
DE VHL86.2-D-3-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6;
RC Kozono Y., Kozono H., Azuma T.:
RT Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067787; BAB63272.1;
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9: 1.
FT NON_TER 145
FT SEQUENCE 145 AA; 13996 MW; 35B1A36E4280BA81 CRC64.

Query Match 74.28; Score 459.5; DB 11; Length 145;
Best Local Similarity 71.78; Pred. No. 4.9e-38;
Matches 86; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

Qy 1 EVQLQSGPELVKPTSVRIKSGTGYTFYTHVWVQSHKSKLEINGNPNNGTGY 60
Db 1 OVQLQSGPELVKPGASVLSKASGYTFYSYWHVWVQRQGLEINGNPNNGTGY 60

Qy 61 NQKFEKATLVTKSSSTAYMELRSITSDESAVYTCAG----WFDVWGQGLTVSS 115
Db 61 NEKFKSKATLVTKSSSTAYMELRSITSDESAVYTCARGLYDGNWFDVWGQGLTVSS 120

RESULT 10
Q924R6 PRELIMINARY: PRT: 137 AA.
AC Q924R6 1
DT 01-DEC-2001 (T:EMBLrel. 19, Created)
DT 01-DEC-2001 (T:EMBLrel. 19, Last sequence update)
DE VHL86.2-D-3-C mu protein (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6;
RC Kozono Y., Kozono H., Azuma T.:
RT Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067783; BAB63268.1;
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9: 1.
FT NON_TER 137
FT SEQUENCE 137

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SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A124 CRC64;

Query Match 74.18; Score 458.5; DB 11; Length 137;
Best Local Similarity 74.87; Pred. No. 5.6e-38;
Matches 80; Conservative 11; Mismatches 15; Indels 3; Gaps 1;

Qy 1 EVQLQSGPELVKPTSVRIKSGTGYTFYTHVWVQSHKSKLEINGNPNNGTGY 60
Db 1 OVQLQSGPELVKPGASVLSKASGYTFYSYWHVWVQRQGLEINGNPNNGTGY 60

Qy 61 NQKFEKATLVTKSSSTAYMELRSITSDESAVYTCAGNPNWFDVWGQGLTVSS 115
Db 61 NEKFKSKATLVTKSSSTAYMELRSITSDESAVYCA---RDVWGQGLTVSS 112

RESULT 11
Q921K1 PRELIMINARY: PRT: 278 AA.
AC Q921K1 1
DT 01-DEC-2001 (T:EMBLrel. 19, Created)
DT 01-DEC-2001 (T:EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T:EMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.:
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC012207; AAH12207.1;
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9: 2; 29778 MW; P894F955DDCD948A CRC64.
SQ SEQUENCE 278 AA; 29778 MW; P894F955DDCD948A CRC64.

Query Match 74.18; Score 458.5; DB 11; Length 278;
Best Local Similarity 70.84; Pred. No. 1.4e-37;
Matches 85; Conservative 12; Mismatches 18; Indels 5; Gaps 1;

Qy 1 EVQLQSGPELVKPTSVRIKSGTGYTFYTHVWVQSHKSKLEINGNPNNGTGY 60
Db 20 OVQLQSGPELVKPGASVLSKASGYTFYSYWHVWVQRQGLEINGNPNNGTGY 79

Qy 61 NQKFEKATLVTKSSSTAYMELRSITSDESAVYTCAGN----FDVWGQGLTVSS 115
Db 80 NEKFKSKATLVTKSSSTAYMELRSITSDESAVYTCRGYDGVDFVWGQGLTVSS 139

RESULT 12
Q8VCV5 PRELIMINARY: PRT: 481 AA.
AC Q8VCV5 1
DT 01-MAR-2002 (T:EMBLrel. 20, Created)
DT 01-MAR-2002 (T:EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T:EMBLrel. 21, Last annotation update).
DE Hypothetical protein, Mus musculus.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC ISSUP-MAMMARY TUMOR;
RC Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC018455; AAH18455.1;
DR InterPro: IPR003599; I9;
DR InterPro: IPR003597; I9_C1.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_MHC.
DR Pfam: PF00047; I9: 4.
DR SMART: SMO0409; I9; 3.

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RC STRATIN=C57BL/6;
KOZONO Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AB067788; BAB63273.1; -.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR00047.1; I.
FT NON_TER 140 140
FT SEQUENCE 140 AA; 15361 MW; 60739B790FC5AF2A CRC64;

Query Match 73.3%; score 454; DB 11; Length 140;
Best local Similarity 73.0%; Pred. No. 1.7e-37;
Matches 84; Conservative 12; Mismatches 16; Indels 0; Gaps

OY 1 EVLOQSGPELVKPGTSVYRSCKTSQFTTEYTHHWKSHGSKSLKLEWGINFNNGCTTY 60
DB 1 OVQLQAPGAEVLKPGASVKLSCKASGTTFTSYVHWVVKVQKRGLEWIGRIDFNSGCTKY 60
OY 61 NQKFEDKATITVDKSSSTAYMEIRLSLTSSEDSANYVYCAAGWFDYGGGTTLTVSS 115
DB 61 NEKFKSRATITVDKPSSTAYMQLSLTSSEDSANYVYCAITAGTWGQGVSTVSS 115

RESULT 15
Q924P5 PRELIMINARY: PRT; 144 AA.
ID- Q924P5
AC Q924P5;
DC 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 1-DEC-2001 (TREMblrel. 19, Last annotation update)
DE VH186_2-D-7-C mouse protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID:10090;
RN [1]
RS SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RA "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AB069920; BAB63936.1; -.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR00047.1; I.
FT NON_TER 144 144
FT SEQUENCE 144 AA; 15865 MW; CD07BE97E9C51B27 CRC64;

Query Match 73.2%; score 453; DB 11; Length 144;
Best local Similarity 71.4%; Pred. No. 2.1e-37;
Matches 85; Conservative 12; Mismatches 16; Indels 4; Gaps

OY 1 EVLOQSGPELVKPGTSVYRSCKTSQFTTEYTHHWKSHGSKSLKLEWGINFNNGCTTY 60
DB 1 OVQLQAPGAEVLKPGASVKLSCKASGTTFTSYVHWVVKVQKRGLEWIGRIDFNSGCTKY 60
OY 61 NQKFEDKATITVDKSSSTAYMEIRLSLTSSEDSANYVYCAAGWFDYGGGTTLTVSS 115
DB 61 NEKFKSRATITVDKPSSTAYMQLSLTSSEDSANYVYCAAGWFDYGGGTTLTVSS 115

Search completed: July 21, 2003, 13:35:07
Job time : 51.7658 secs

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